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Title:
Perfect score:
Sequence:
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Maximum
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 112
12
13
14
16
16
18
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Sp_archea:*

sp_archea:*

sp_bacteri7

sp_fung1:*

sp_human:

sp_human:

sp_human:

sp_manm/
rsp_manm/
rsp_manm/
sp_mbcrc
esp_ph
10: sp_b
11: sp
12: sr
13: g
14:
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DB
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sp_unclassified:*
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1 Q99K94
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3 Q9DDJ8
3 Q93599
3 Q13133
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      Oggvr4 rattus sp.
Q9bxh2 homo sapien
O13132 oncorhynchu
Q9qvr3 rattus sp.
Q9ud15 homo sapien
Q99k94 mus musculu
O9qxk0 rattus norv
Q9d323 mus musculu
O13131 oncorhynchu
                                                                                                                            O9pvx8 xenopus lae
O9n145 macca mula
O9ddj8 brachydanio
O93599 brachydanio
O13133 oncorhynchu
                                                                                                                     Q9n0j4 bos taurus
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                                                                                                                                                                                             014916 homo sapien
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nomo
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Q85036 porcine rot	055590 avian rotav	P88944 kaposi's sa		Q9jkm1 mus musculu	09dg74 oncorhynchu	Q9hqb3 halobacteri	097164 anopheles g	Q9bqd2 homo sapien	Q9pwp7 gallus gall	Q9rj58 streptomyce	087594 streptomyce	Q9fkiB arabidopsis	Q99ku6 mus musculu	Q9krp8 vibrio chol	Q9n0e5 bos taurus	070429 rattus norv	070406 rattus norv	Q29340 sus scrofa	Q9qze4 mus musculu	Q9qxj2 mus musculu	Q9vy71 drosophila	018168 caenorhabdi	Q9xxe3 caenorhabdi	093598 brachydanio	Q9gky9 sus scrofa

ALIGNMENTS

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HSSP; H42227; IBG1.
HSSP; H42227; IBG1.
/InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 2.
SEQUENCE 770 AA; 88067 M
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014916;
01-JAN-1998
01-AUG-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                           Della Pietra L., Bressan A., P. Submitted (OCT-1997) to the EM EMBL; AJ012463; CAA10032.1; -. EMBL; AF029311; AAB84254.1; -.
                                                                                                                                                                SEQUENCE OF 564-704 FROM N.A. TISSUE-HEPATOMA;
                                                                                                                                                                                                                                                                                          STAT3
                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSCRIPTION FACTOR (SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION
                                                                                                                                                                                                        Della Pietra L., Bressan A., Pezzotti
"Highly conserved amino-acid sequence
revised human STANT3 sequence.";
Gene 213:119-124(1998).
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98296260; PubMed-9630560;
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     MW.
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                                                                                                                                                    Pezzotti A.R.,
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     6C00632211C8012D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     770
                                                                                                                                                                                                                                   A., Serlupi-Crescenzi O.; between murine STAT3 and
                                                                                                                                                   Serlupi-Crescenzi O.;
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Query Match
Best Local Similarity
Matches 732; Conserv

Conservative

0

Mismatches

2;

0,

Gaps

0;

69.18; 99.78;

Score 532; Pred. No. 0;

DB 4;

Length 770; Indels

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RESULT
ID BW54
AC OS
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TISSUE-KIDNEY ADENOCA
Y Strausberg R.;
Submitted (NOV-2000) t
EMBL; BC000627; AAH006
SEQUENCE 760
                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pı
NCBI_TaxID=9606;
                                                                                                                                                                                                         O9BW54
O9BW54
O9BW54
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIGNAL TRANSCUCER AND ACTIVATOR OF TRANSCRIPTION 3.
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ADENOCARCINOMA;
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Primates;
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                   MW;
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Catarrhini;
                   A374A32AB9D28077
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                                                     databases
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Best Local S
Matches 673
                                D Q9PVX8 PRELIMINARY; PRT; 769 AA.

C Q9PVX8;

T Q1-MAY-2000 (TrEMBLrel. 13, Created)
T Q1-MY-2000 (TrEMBLrel. 13, Last sequence update)
T Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E STAT 3.
S Xenopus laevis (African clawed frog).
S Xenopus laevis (African clawed frog).
E Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut.
C Eukaryota; Metazoa; Anura; Mesobatrachia; Pipoidea; Pij
Xenopodinae; Xenopus.
N CSI_TaxID-8355;
SEQUENCE FROM N.A.
Nishinakamura R., Mat
Asashima M., Yokota 1
"Activation of Stat3
                                                                                                                                                                                                                                                                                                                                                                                                               146
                                                                                                                                                                  686
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                                                                                                                                                                                                                                                                                                                                                              WITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFYVVEK
                                                                                                                                                                              673;
                                                                                                                                                           YCRPESQEHPEADPG
                                                                                                                                                    YCRPESQEHPEADPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
              Matsumoto
Т.;
в by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.48;
99.78;
                                                                                                                                                    700
cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 473;
Pred. No. 0
              Υ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
              Matsuda
receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
              ₹.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
gp130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
              Ariizumi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
 ventralizes
                                                  Euteleostomi; Pipidae;
               Heike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                  505
                                                                                                                                                                                                                                                                                                445
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                                                                                                                                                                                                                                                                                                                                                                                                                  205
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embryos independently of BMP-4."; Dev. Biol. 0:0-0(1999). EMBL; AB017701; BAA86061.1; -. HSSP; P42227; 1BG1.

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RESULT
OPNILET
AC OF OPNILET
O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
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                                       Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QY
  밁
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Best Loc
Matches
                                                                                   Query Match
Best Local S
Matches 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR000980; SH2.
Interpro; IPR001217; STAT
Pfam; PF00017; SH2: 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2: 1.
PROSITE; PS50001; SH2: 1.
PROSITE; PS50001; SH2: 1.
SEQUENCE 769 AA; 87974
                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Arredondo J.;
Arredondo J.;
Transduction Genes from Rhesu
"Cytokine Signal Transduction Genes from Rhesu
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF227560; AAF73401.1; -
Interpro; IPR001217; STAT.
Pfam; PF01017; STAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9N145;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (FRAGMENT)
STAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9544;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9N145
                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468
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                                            249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match
Local Similarity
nes 271; Conserv
    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPNAWASILMYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FISKERERAILSTKPPGTFLLRFSESSKEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISKERERAILSTKPPGTFLLRFSESSKEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAE
IACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEER 308
                                                                                      al Similarity
145; Conserv
                                                                                                                                                                                                 163 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.2%;
llarity 100.0%;
Conservative (
                                                                                   18.8%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                   ÀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca.
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                                                                                                                                                                                                   18855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH2.
STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 271; DB; Pred. No. 1.4:0; Mismatches
                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                        Score 145; DB 6; L
Pred. No. 2.6e-145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0905C03263303069 CRC64;
                                                                                                                                                                                                   DD3F11E7F5B9878C
                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4e-278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                   Rhesus Macaques.";
/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                             Length 163;
                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels ·
                                                                                        Indels
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                                                                                        0;
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                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                        0;
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RESULT Q9DDJ8
ID DQ9
ID Q9
DT 01
DT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    γΩ
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  RESULT
093599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zebrafish to Mouse.";
Genomics 0:0-0(2001).
EMBL; AF3228:7; AAG42495.1;
InterPro; IP: 010980; SH2.
InterPro; IP: 010917; STAT.
Pfam; PF01017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Zebra danio).

Bukaryota; Metazoa; Chordata; Craniata; Verte

Actinopterygii; Neopterygii; Teleostei; Eutel

Cypriniformes; Cyprinidae; Rasborinae; Danio.

NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9DDJ8 PRELIMINARY; PRT; 394 AA.
Q9DDJ8:
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSCRIPTION FACTOR STAT3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                 O93599 PRELIMINARY;
093599;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Miyoshi K., Cui Y., Ried
Oka T., Dewar K., Hennig
"Structure of the Mouse
                                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                         STAT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAT3
Oates A.C.;
Thesis (1998), University of
EMBL; AJ005693; CAA06677.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597
                                                                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKDSGDVAALRGSRKFNILGTNTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63: Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.2%; ilarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                )1; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hennighausen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Riedlinger G.,
Hennighausen L.;
Mouse Stat 3/5 Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44126 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 63;
Fred. No.
                                                                                                                                                                                                                                                                      Last sequence up
                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                     Melbourne,
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2BDEDFE716B50E70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                               806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
7.7e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi
                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ostariophysi;
                                                                                                                                                           Ostariophysi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT
013133
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                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЬ
                                                                                                                                                                                                            Query Match
Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P42227; 1BG1.
Interpro; IPRO00980; SH2.
Interpro; IPRO01217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 806 AA; 92151 M
                                                                                                                                                                                                                                                            InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SEQUENCE 767 AA; 87816 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                 013133
013133;
01-JUL-1997
01-JUL-1997
01-JUN-2001
                                                           Q9NOJ4 PRELIMINARY; PRT; 56 AA.
Q9NOJ4;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3,
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Johnson M.C., Mourich D.V.,
Submitted (JUN-1996) to the
EMBL; U60333; AAB60926.1; -
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                     Oncortynchus mykiss (Rainbow trout) (Salmo gairdneri). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E. Actinopterygii; Neopterygii; Teleostel; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorh NCBI_TaxID=8022;
                   Eukaryota; Metazoa;
Mammalia; Eutheria;
 Bovidae; Bovinae; NCBI_TaxID=9913;
                              Eukaryota;
                                                    STAT3
                                           Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                               RBTSTAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                          STAT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537
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                                                                                                                                                                                                             Local Similarity les 59; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 8.2%;
Similarity 100.0%;
63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 04, (TrEMBLrel. 04, (TrEMBLrel. 17,
                                                                                                                                                                                                          7.7%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
            Bos.
                      Chordata; Craniata; Vertebra Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                              87816 MW;
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                                                                                                                                                                                                            0,
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                    Leong J.C.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                          Score 59; DB
Pred. No. 2.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 6
                                                                                                                                                                                                                                                             FED97740C74C3798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74BC4EA401C3C942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                              J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            767
                                                                                                                                                                                                                    DB 13; 1
2.5e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; I
1.5e-57;
                    Vertebrata; Eute minantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
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                                                                                                                                                                                                                             Length 767;
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                                                                                                                                                                                                                                                                                                                                                                                     Oncorhynchus
                                                                                                                                                                                                            Indels
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                              Euteleostomi;
                                                             STAT3 (FRAGMENT)
                      Bovoidea:
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RESULT
Q99ML3
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Best Local S
Matches 56
                                                                                                                                                                                                                   Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                             Q99ML3;
Q1-JUN-2001 (TrEMBLrel. 1
Q1-JUN-2001 (TrEMBLrel. 1
Q1-JUN-2001 (TrEMBLrel. 1
STAT3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The STAT3-encoding gene resides within the 40 kbp gap 1 STAT5A- and STAT5B-encoding genes in cattle."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ276489; CAB93140.1; Interpro; IPR001217; STAT. Pfam; PF01017; STAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
Molenaar A., Wheele
                                                                                                                 Q9QVR4
Q9QVR4;
01-MAY-2000
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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"Murine Stat3 gene exon 22 t
Submitted (DEC-2000) to the
EMBL; AF332507; AAK17195.1;
     SEQUENCE FROM N.A.
MEDLINE-95398099; PubMed-7545365;
MEDPLINE-95398099; PubMed-7545365;
Kipperger J., Fritz S., Richter K
Lochner K., Marschalek R., Hocke
                                                 Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10118;
                                                                              Rattus sp.
                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTERLEUKIN-6 RESPONSE ELEMENT BINDING PROTEIN (FRA
                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99ML3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                    ch 6.6%; l similarity 100.0%; 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 7.3%;
l Similarity 100.0%;
56; Conservative (
                                                                                                                                                                                                                                                                                                                              FROM N.A
                                                                                                                                                                                                                                                                                                                                                        lus (Mouse).
; Metazoa; Chordata;
Eutheria; Rodentia;
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    Marschalek
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                                                                                                                                    PRELIMINARY;
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5379
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                                                           Chordata;
Rodentia;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                    Score 51; DB
Pred. No. 6.9
0; Mismatches
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                                                          Craniata; Vertebrata; Sciurognathi; Muridae;
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Sciurognathi; Muridae;
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     Dreier B., :
, Lottspeich
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                                                            Muridae;
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     Schneider
1 F., Fey (
                                                                                       (FRAGMENT)
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                                                           Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                            Murinae;
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RESULT
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ID 3132
ID 3132
ID 317
O1 DT 01
DT 01
OT 01
OC 07
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Best Local S
Matches 38
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Best Loc
Matches
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01-JUL-1997
01-JUL-1997
01-JUN-2001
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01-JUN-2001
01-JUN-2001
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"Human S
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SEQUENCE
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Ann. N. Y. Acad. Sci. 7
HSSP; P4/227; 1BG1.
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                             SEQUENCE FROM N.A.
Johnson M.C., Mourich D.V.,
Submitted (JUN-1996) to the
EMBL; U60332; AAB60925.1; ...
HSSP; P42224; 1BF5.
                                                                                                                                                                                                                                          Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Protacanthopterygii; Meopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorh
                                                                                                                                                                                                                                                                                                                                                                     RBTSTAT1-2
                                                                                                                                                                                                                                                                                                                                                                                                         STAT1-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                NCBI_TaxID=8022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        702
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nes 38; Conser
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n STAT3 gene exon 22 to
tted (DEC-2000) to the E
AF332508; AAK17196.1;
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   IPR000980;
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(TrEMBLrel. 04,
(TrEMBLrel. 17,
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(TrembLrel. 17, Last seq
(TrembLrel. 17, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.98; ilarity 100.08; Conservative
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5375
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Primates;
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100.0%;
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Last sequence up
Last annotation
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                                                                                           Leong J.C.;
EMBL/GenBank/DDBJ
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Pred. No.
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1.9e-37;
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Q9QVR3;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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SEQUENCE
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SO DR
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Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART: SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 754 AA; 87147 MW;
SEQUENCE FROM N.A. MEDLINE=92346719; I FU X.Y.; FU X.Y.; A transcription for an interferon a kinase(s).";
                                                                                                                                                                                                               Q9UDL5
Q9UDL5;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTERFERON-STIMULATED GENE FACTOR 3 ALPHA 91/84 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95398099; PubMed=7545365;
MEDLINE-95398099; PubMed=7545365;
Mipperger J., Fritz S., Richter K., Dreier B., Schneider K.,
Ripperger J., Fritz S., Richter K., Dreier B., Schneider K.,
Lochner K., Marschalek R., Hocke G., Lottspeich F., Fey G.H.;
"Isolation of two interleukin-6 response element binding proteins acute phase rat livers.";
Ann. N.Y. Acad. Sci. 762:252-260(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10118;
                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTERLEUKIN-6 KESPONSE ELEMENT BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00017; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000980; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P42224; 1BF5
                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      585 IMGFISKERERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 RKFNILGINTKVMNMEESN
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12; Conser
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19; Conser
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PS50001; SH2; 1.
43 AA; 4937 MW;
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                 factor with SH2 and SH3 domains is directly alpha-induced cytoplasmic protein tyrosine
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                                                                          PubMed=1638633
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Rodentia;
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Primates;
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100.0%
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5D710A6749125C3B CRC64;
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                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
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0.00016;
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7.8e-11
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RESULT 15
Q99K94
ID Q99K94
AC Q99K94
AC Q99K94
DT 01-JUN
DT 01-JUN
DT 01-JUN
DT SIMILA
OS MUS mu
OC EUKARY
OC Mammal
OX NCBI_T
RN (1)
RP SEQUEN
RA Straus
RL EMBL;
SQ SEQUEN
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Search completed: March 19, 2002, 15:27:46 Job time: 243 sec
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                                                                                                                                                   Query Match 1.6%; Score 12; DB 11; Length 712; Best Local Similarity 100.0%; Pred. No. 0.002; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 70:323-335(1992).
HSSP; P42224; 1BF5.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF001017; SH2; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
NON_TER 1
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Q99K94;
Q99K94;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.
Mus musculus (Mouse).
EUKarryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
McBI_TaxID=10090;
[1]
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004808; AAH04808.1; .
SEQUENCE 712 AA; 83106 MW; D62081709638CDA5 CRC64;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          585 IMGFISKERERA 596
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60 IMGFISKERERA 71
                                                                                    585 IMGFISKERERA 596
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578 IMGFISKERERA 589
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156
156 AA;
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156
18004 MW; 4D6E4D7D353C0AAA CRC64;
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Run on:
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March 19, 2002, 15:22:48; Search time 14.48 Seconds (without alignments) 1949.718 Million cell updates/sec
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Title: Perfect score: Sequence: US-08-212-185-12 770

1 MAQWNQLQQLDTRYLKQLHQ.....QFESLTFDMDLTSECATSPM 770

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7 0.9 94 1 SPDA_STRLI 7 0.9 128 1 YF70_AQUAE 7 0.9 136 1 SR14_HUMAN 7 0.9 161 1 CC31_YEAST 7 0.9 170 1 Y586_METJA 7 0.9 173 1 PSAL_MASLA 7 0.9 173 1 PSAL_MASLA 7 0.9 205 1 MD21_HUMAN 7 0.9 205 1 MD21_HUMAN 8 0.9 205 1 MD21_HUMAN 9 0.9 2	94 1 128 1 161 1 170 1 173 1 173 1 193 1 205 1 205 1 209 1 238 1	45	44	43	42	41	40	39	38	37	36	35	34
94 1 128 1 161 1 170 1 173 1 173 1 193 1 205 1 205 1 209 1 238 1	94 1 SPDA_STRLI P22407 128 1 YF70_AQUAE 07514 136 1 SR14_HUMAN P37108 161 1 CC31_YEAST 058006 170 1 Y586_METJA 051126 173 1 PSAL_MASLA 051126 173 1 PSAL_MASLA 051126 173 1 PSAL_MASLA 051226 173 1 PSAL_MASLA 051226 205 1 MD21_HUMAN 0252 205 1 MD21_HUMAN 025255 205 1 YRBK_HAEEN 092155 201 1 ERG2_MAGGR P33281 238 1 AGRA_STAAU P13313	7	7	7	7	7	7	7	7	7	7	7	7
	1 SPDA_STRLI P22407 1 YFTO_AGUAE P2707 1 YFTO_AGUAE P37108 1 SR14_HUMAN P37108 1 CC31_YEAST P06704 1 Y586_METJA P06704 1 Y586_METJA P06704 1 P5AL_MASLA P4809 1 P631_DROME P4809 1 P631_DROME P4809 1 MD21_HUMAN P1851 1 MD21_MOUSE P45075 1 YRBK_HAEIN P133281 1 AGRA_STAAU P133131	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9
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SPDA_STRLI YF70_AQUAE SR14_HUMAN CC31_YEAST Y586_METJA PSAL_MASLA E631_DROME MD21_HUMAN MD21_HUGAN MD21_MOUSE YRBK_HAELN ERG2_MAGGR AGRA_STAAU	P22407 067514 P37108 P06704 Q58006 O41126 P4893 Q13257 Q921b5 P45075 P332815	۲	۲	ר	ب	<u>س</u>	1	_	1	_	1	1	_
		AGRA_STAAU	ERG2_MAGGR	YRBK_HAEIN	MD21_MOUSE	MD21_HUMAN	E631_DROME	PSAL_MASLA	Y586_METJA	CC31_YEAST	SR14_HUMAN	YF70_AQUAE	SPDA_STRLI

ALIGNMENTS

	RESULT AC DIT O DIT O DIT O O O O O O O O O O O O O O O O O O O
Cell 77:63-71(1994). [2] SEQUENCE FROM N.A. TISSUE=Thymus; MEDLINE=94188718; Pubm Zhong Z., Wen Z., Darn "Stat3: a STAT family response to epidermal Science 264:95-98(1994) SEQUENCE FROM N.A. TISSUE=Brain; MEDLINE=95014185; Pubm Raz R., Durbin J.E., L "Acute phase response interferon-stimulated from cytokines, interf J. Biol. Chem. 269:243 SEQUENCE FROM N.A. (ST STRAIN=BALB/C, AND B6; MEDLINE=96016116; Pubm SCHAEFER T.S., Sanders "Cooperative transcrip form of Stat3."; PIOC. Natl. Acad. Sci. [5] PHOSPHORYLATION OF SER MEDLINE=95354205; Pubm "Maximal activation of tyrosine and serine ph cell 82:241-250(1995).	OUSE TA3_MOUS 42227; 1-NOV-19 1-OCT-19
pubMed=814, Darmell J. Darmell J. Darmell J. Darmell J. Darmell J. Darmell J. PubMed=752 E., Levy D. Onse factor acted gene factor pubMed=754, barnell J. Darnell J. Darnell J. Darnell J. Gene gene gene gene gene gene gene gene	PE STANDARD; P. 195 (Rel. 32, Created) 196 (Rel. 34, Last sequence) 101 (Rel. 40, Last announce) 101 (Rel. 40, Last announce) 102 (Rel. 40, Last announce) 103 (Rel. 40, Last announce) 104 (Rel. 34, Last sequence) 105 (Rel. 40, Last announce) 106 (Rel. 34, Last sequence) 107 (Rel. 40, Last announce) 108 (Rel. 32, Created) 108 (Rel. 32, Created) 109 (Re
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nd by tyrosine phosphorylation in nod interleukin-6."; tional members of the amily integrate diverse signals th factors."; of Jun and Stat3 beta, a short -9101(1995). ENESIS. ENESIS. by Stat1 and Stat3 requires both;	AA. (e) (ate) (ate) (arprion 3 (ACUTE-PHASE) (i; Muridae; Murinae; Mus. (58; 181-185 AND 632-640. (58; 181-185 AND 632-640. (58) T.; (57.; (57.; (58) T.; (58) T.; (58) Matsusaka T., (58) T.; (58) T.; (58) Matsusaka T., (58) T.; (59) T.; (59) T.; (50) T.;

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Best Local Sim
Matches 743;
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InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
                                                                                                CONFLICT
CONFLICT
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SEQUENCE
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VARSPLIC
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PDB; 1BG1;
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                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                        MUTAGEN
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X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF
MEDLINE=98334373; PubMed=9671298;
Becker S., Groner B., Mueller C.W.;
                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                Phosphorylation;
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                                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                           ranscription
                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:103038; Stat3
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                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LESS ABUNDANT MANNER.

PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-ALPHA AND OSM. SERINE PHOSPHORYLATION IS IMPORTANT FOR THE FORMATION OF STABLE DNA-BINDING STAT3

HOMODINERS AND MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.

SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE INTERLEUKIN-6 (IL-6) RESPONSIVE ELEMENTS IDENTIFIED IN THE PROMOTERS OF VARIC ACUTE-PHASE PROTEIN GENES. STAT3B INTERACTS WITH THE N-TERMINAL PART OF C-JUN TO ACTIVATE SUCH PROMOTERS IN A COOPERATIVE WAY. PATHWAY: INVOLVED IN THE GP130 MEDIATED SIGNALING PATHWAY. SUBUNIT: FORMS A HOMOLINER OR A HETERODIMER WITH A RELATED FAMI MEMBER (AT LEAST STAT1) (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR: TRANSLOCATED INTO THE NUCLEUS IN RESPONSE TO PHOSPHORYLATION.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; STAT3A (SHOWN HERE) AND STAT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: STAT3A IS SEEN IN
KIDNEY. STAT3B IS ALSO DETECTED IN TH
                                                                                                                                                                                                                                                                                                                                                                                L; L29278; AAA37254.1; -.
; U06972; AAA19452.1; -.
; U08378; AAA56668.1; -.
; U30779; AAC52612.1; -.
1BG1; 13-JAN-99.
FPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQQYSRFLQESNVLYQHNLRR 85
                                                 Similarity
                                                                                                                                                                                                                                                                                      M00252; SH2; 1.
PS50001; SH2; 1.
                                                                                             16
25
394
770
                                      Conservative
                                                                                                                                                        701
                                                                                                                                                                                                                                                regulation; DNA-binding; Nuclear protein; on; Alternative splicing; 3D-structure.
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25
394
88053
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705
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727
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STAT3B).

STAT3B).

MISSING (IN SOME S->A: DECREASED T ACTIVATION.

E -> K (IN REF. 2
S -> T (IN REF. 2
S -> I (IN REF. 1
I (IN REF. 1)
                                   Score 543; DB Pred. No. 0; 0; Mismatches
                                      0;
                                                                                                                                                                                                  SIMILARITY).
PHOSPHORYLATION.
TTCSNTIDLPHSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                                                                                                                                                                                                       PHOSPHORYLATION
                                                                                            -> K (IN REF. 2).

-> T (IN REF. 2 AND 4).

-> I (IN REF. 1).

6C00626711C8012D CRC64;
                                                543; I
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2 AND 4).
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Rattus norvegicus (Ra
Eukaryota; Metazoa; C
Mammalia; Eutheria; I
NCBI_TaxID=10116;
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01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
01-NOV-1997 (Rel. 3
SIGNAL TRANSDUCER A
STAT3.
           Ripperger J.A., Fritz S., Richter K., Hc
Fey G.H.,
"Transcription factors Stat3 and Stat5b
nuclei late in an acute phase response a
                                                MEDLINE=96102059; Publ
Ripperger J.A., Fritz
                                                                          SEQUENCE FROM
TISSUE=Liver;
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ritz S., Richter
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Last sequence update)
Last annotation updat
ACTIVATOR OF TRANSCRI
                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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             and
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InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
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between
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   672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESPONSE TO PHOSPHORYLATION (BY SIMILARITY).

RESPONSE TO PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF, PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-ALPHA AND OSM. SERINE PHOSPHORYLATION IS IMPORTANT FOR THE FORMATION OF STABLE DNA-BINDING STAT3 HOMODIMERS AND MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.

SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.
SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAMILY
MEMBER (AT LEAST STAT1) (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE INTERLEUKIN-6 (IL-6)-RESPONSIVE ELEMENTS IDENTIFIED IN THE PROMOTERS OF VARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IL-6)-RESPONSIVE ELEMENTS IDENTIFIED ACUTE-PHASE PROTEIN GENES.
VTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVN
                                                                                                                                                                                                                                                                                                                            SGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGNGGRANCDASLI 431
                                                                                                                                                                                                                                                                                                                                                                                        LFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCIDKD
                                                                                                                                       ENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFS
                                                                                                                                                                                                     FFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYSGCQITWAKFCK
                                                                                                                                                                                                                                                                                                            YLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSNTIDLPMSPRTL
                                                                                                                          ENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFS
                                                                                                                                                                                      FFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYSGCQITWAKF~K
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770
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PHOSPHORYLATION (BY SIMILARITY).
D74A0C76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 459;
Pred. No.
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                                                                           Pfam; PF00017; SH2; 1. Pfam; PF01017; STAT; 1. SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T.; Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 pyl-related transcription factor involved in the gpl30-mediated signaling pathway.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAT3 on .... Homo sapiens (Human).

Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, SIGNAL TRANSDUCER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995
01-FEB-1995
  Transcription regulation; D
Phosphorylation; SH2 domain
                                                                                                                                                                                                                    MIM; 102582;
                                                                                                                                                                                                                                       HSSP; P42224; 1BF5.
TRANSFAC; T01493; -.
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Cell 77:63-71(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
MEDLINE=94208062; PubMed=7512451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAT3 OR APRE
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                                                     PROSITE; PS50001; SH2; 1.
                                                                                                                                                            InterPro; IPR000980;
InterPro; IPR001217;
                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95215843;
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TISSUE SPECIFICITY: HEART, BRAIN, PLACENTA, LING, LIVER, SKELETAI MUSCLE, KIDNEY, AND PANCREAS.

PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO 11-6, 11-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN ALPHA AND OSM. SEKINE PHOSPHORYLATION LIF, CSF-1, EGF, PDGF, IFN ALPHA AND OSM. SEKINE PHOSPHORYLATION OF STABLE DNA-BINDING STAT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMODIMERS AND MAXIMAL TRANSCRIPTIONAL ACTIVITY.
SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACUTE-PHASE PROTEIN GENES.

PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.

SUBGUNT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAMIL
MEMBER (AT LEAST STAT1).

SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO (IL-6)-RESPONSIVE ELEMENTS IDENTIFIED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X., Flenis J., Li H.-C., Schindler C., Chen-Kiang irem '' secine phosphorylation for formation of
                                                                                                                                                                                                                                                                                            L29277; AAA58374.1;
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31,
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                                                                                                                                                            SH2.
STAT
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Last annotation updat
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                         DNA-binding; Nuclear protein;
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STAT-promoter
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                                                               RT ACLIVATORS OF TRANSCRIPTION.";

RP PTOC. Natl. Acad. Sci. U.S.A. 91-KHOLL 1015-100-11-1016

C: PROCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE IEN-STIMULATED COMMENT. TRANSCRIPTION FACTOR THE GAS ELEMENT. THIS MULTIPROTEIN COMMENT. IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STAT1-COMMENT. IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STAT1-COMMENT. IN RESPONSE TO IFN NALPHA/BETA, THREE SUBUNITS (STAT1-COMMENTARIA) OF ISCF3, BECOME PHOSPHORYLATED ON TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX COMMENTARIA (P48), A DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT. IN RESPONSE TO IFN GAMMA, STAT1 FORMS HOMODIMERS, THAT ALSO TRANSLOCATE INTO THE NUCLEUS TO ACTIVATE IFN GAMMA-RESPONSIVE GENES. INTERACTS WITH NMI (BY SIMILARITY).

C: SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN RESPONSE TO PHOSPHORYLATION.

C: INDUCTION: BY IFN AND EGF.

C: PIM: TYROSINE PHOSPHORYLATED IN RESPONSE TO FIN-ALPHA, DEFF. SERINE PHOSPHORYLATION IS ALSO REQUIRED FOR MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY).

C: SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.

C: INDUCTIONS OF THE STAT FAMILY OF TRANSCRIPTION FACTORS.
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Best Local S
Matches 221
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01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
20-AUG-2001 (Rel. 4
SIGNAL TRANSDUCER A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _MOUSE
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SEQUENCE
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MOD_RES
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STA1_MOUSE
                                                                                                                                                                                                                                                                                                                                                              Zhong Z., Wen Z., Darnell J.E. Jr.;
"Stat3 and Stat4: members of the family of signal transducers
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94255416; PubMed=7545930;
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLE
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770
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705
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Rodentia;
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100.0%;
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PHOSPHORYLATION
SIMILARITY).
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A3DCEE815B3B5360
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             and the EMBL outstation are no restrictions on it
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; Murinae; Mus
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InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
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01-NOV-1995
01-NOV-1997
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        Yan R., Qureshi S., Zhong Z., Wen Z., Darnell J.E. Jr.;
"The genomic structure of the STAT genes: multiple exon:
coincident sites in Statl and Stat2.";
Nucleic Acids Res. 23:459-463(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 514-524; 654-1 MEDLINE-92366557; PubMed-1502203; Schindler C., Fu x.-Y., Improta T., Aebersold R., *Proteins of transcription factor ISGF-3; one general edges o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2000 (Rel. 40, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                   "Phosphorylation and activation of t
purified Stat! by the Janus protein-
epidermal growth factor receptor",
J. Biol. Chem. 270:20775-20780(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STAT1
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   MEDLINE=95354205;
Wen Z., Zhong Z.,
                                                                                                                                                                                                                                                                           Quelle F.W.,
                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION OF TYR-701.
MEDLINE=95386533; PubMed=7657660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE FROM N.A. MEDLINE=95192056; PubMed=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STA1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires
                                                         PHOSPHORYLATION OF SER-727, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                    Ihle J.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation;
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12; Conserv
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                                                                                                                                                                                                                                                                           Thierfelder W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=7885841;
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   Darnell
                                   PubMed=7543024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      727
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100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                           Witthuhn
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Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514-524; 654-660 AND 667-672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          750
                                                                                                                                                                                                                                                                           B.A.,
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InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM0052; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U18663; -; EMBL; U18664; -; EMBL; U18665; -; EMBL; U18666; -; EMBL; U18666; -; EMBL; U18668; -; EMBL; U18669; -; EMBL; 
CONFLICT
SEQUENCE
                                                                               MOD_RES
MOD_RES
VARSPLIC
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98292180;
Chen X., Vinkemei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Maximal activation of transcription by Statl and Stat3 requires both tyrosine and serine phosphorylation."; Cell 82:241-250(1995).
                                                                                                                                                                                    Transcription regulation; DNA-binding; Phosphorylation; SH2 domain; Alternativ DOMAIN 573 670 SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 600555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS RESPONSE TO PHOSPHORYLATION.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA/P91 (SHOWN HERE) AND BETA/P84; ARE PRODUCED BY ALTERNATIVE SPLICING.
PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IFN-GAMMA, IFN-AL PDGF, AND EGF. SERINE PHOSPHORYLATION IS ALSO REQUIRED FOR MATRANSCRIPTIONAL ACTIVITY (LACKING IN BETA FORM).
SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTOSIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: IFN-SIGNALLING PATHWAY:
SUBUNIT: IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STATI-
SUBUNIT: IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STATI-
ALPHA, STATI-BETA, STATI) OF ISGF, BECOME PHOSPHORYLATED ON
TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX
TOGETHER WITH ISGF3 GAMMA (P48), A DNA-BINDLING PROTEIN THAT
SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT. IN
RESPONSE TO IFN GAMMA, STATI FORMS HOMODIMERS, THAT ALSO
TRANSLOCATE INTO THE NUCLEUS TO ACTIVATE IFN GAMMA-RESPONSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (ISRE) AND TO THE GAS ELEMENT. THIS MULTIPROTEIN TRANSCRIPTION FACTOR IS TERMED ISGF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENES. INTERACTS WITH NMI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93:827-839(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1BF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      м97935;
м97936;
                                                                                                                                                                                                                                                                   PS50001; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        T01492;
261
750 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB64012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOT_ANNOTATED_CDS
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  271
87334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a tyrosine phosphorylated STAT-1 dimer bound
  MW.
                               MISSING
                                                                               MISSING (IN ISOFORM BETA)
S->A: DECREASED TRANSCRIP
                                                                                                                                 PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                              Alternative
054A813522364BA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jeruzalmi D., Darnell J.E.
                               (IN M97936)
                                                                                                                                                                                                                                          Nuclear protein;
                                                                                                                                                                                                                 splicing; 3D-structure
                                                                            TRANSCRIPTIONAL
                                                                                                                                                           (BY JAKS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFN-ALPHA,
FOR MAXIMAL
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Best Local S
Matches 12
                                               Best Lo
                                                                       Query Match
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Q14765;
30-MAY-2000
                                                                                                             MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and confers selective sequence recognition.*;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CARRIES OUT A DUAL FUNCTION: SIGNAL TRANSDUCTION AND
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL TRANSDUCER
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30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                            Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                           EMBL; L78440; AAB05605.1; MIM; 600558; -.
                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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                                                                                                                                                MOD_RES
                                                                                                                                                               DOMAIN
                                                                                                                                                                        Transcription regulation; DN Phosphorylation; SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The STAT amino-terminal domain mediates cooperative DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               578
                                                                                                                                                                                                   PROSITE;
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 592
                       603
                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: TYROSINE PHOSPHORYLATED. SERINE PHOSPHORYLATION IS ALSO REQUIRED FOR MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY). SINILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A REMBER (BY SIMILARITY).

NUCLEAR; TRANSLOCATED INTO THE RESPONSE TO PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVATION OF TRANSCRIPTION
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 PGTFLLRFSES
                       PGTFLLRFSES 613
                                               l Similarity 100.0%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
12; Conser
                                                                                                                                                                                                   PS50001; SH2;
                                                                                                                                                                                                                                                IPR000980; SH2. IPR001217; STAT
                                                                                                             721
748 AA;
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602
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39,
39,
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                                                                                                              721
85940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Last annotation updat
ACTIVATOR OF TRANSCRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.68;
                                                                                                              ¥.
                                                                                                                                                                                      DNA-binding; Nuclear protein;
                                                 0;
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Pred. No.
                                               Score 11; DB 1;
Pred. No. 0.0071
0; Mismatches
                                                                                                                          PHOSPHORYLATION
                                                                                                                                      SIMILARITY)
                                                                                                                                                  PHOSPHORYLATION (BY JAKS) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                              11E43803A9AF4FFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                          (BY SIMILARITY)
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                                                                         Length 748
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                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                 a collaboration -
MBL outstation -
                                               0;
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RESULT
STA4_MC
    InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
SIGNAL TRANSDUCER AND ACTIVATOR OF TRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the 2MBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BALB/C; TLSSUE=Testis;
MEDLINE=94277038; PubMed=8007943;
Yamamoto K., Quelle F.W., Thierfelder W.E.,
Gilbert D.J., Jenkins N.A., Copeland N.G., 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94255416; PubMed=7545930; Zhong Z., Wen Z., Darnell J.E. Jr.; "Stat3 and Stat4: members of the family of signal activators of transcription."; Proc. Natl. Acad. Sci. U.S.A. 91:4806-4810(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAT4
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01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                     -!- PTM: TYROSINE PHOSPHORYLATED. SERINE PHOSPHORYLATION IS ALSO REQUIRED FOR MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTOR-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Stat4, a novel gamma interferon activation site-binding protein expressed in early myeloid differentiation."; mol. Cell. Biol. 14:4342-4349(1994).
                                                                                                                                                                                                      EMBL; U06923; AAA19453.1; EMBL; U09351; AAA19692.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAT-4.";
Science 279:1048-1052(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STA4_MOUSE
                                           Phosphorylation; SH2 domain;
                                                       PROSITE; PS50001; SH2; 1.
Transcription regulation; DNA-binding; Nuclear
                                                                                                                                                                          TRANSFAC; T01576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure of the amino-terminal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vinkemeier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98128033; PubMed=9461439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 1-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ihle J.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR; RESPONSE TO PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVATION OF TRANSCRIPTION SUBUNIT: FORMS A HOMODIMER (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CARRIES OUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moarefi I., Darnell J
                                                                                                                                                              Stat4.
                665
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PHOSPHORYLATION SIMILARITY).
                              SH2
                                            3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR A HETERODIMER WITH A RELATED FAMILY
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tion update)
TRANSCRIPTION
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[T]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interaction
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               (BY JAKS)
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                                                        protein;
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RESULT 8
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                          Matches
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Best Local
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STA2_HUMAN STANDARD; PRT; 851 AA.
P52630; Q16430; Q16431;
Q1-OCT-1996 (Rel. 34, Created)
Q1-OCT-1996 (Rel. 34, Last sequence update)
Q0-AUG-2001 (Rel. 40, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 2 (P113).
        This
                                                                                                                                                                                                                                                              Sugiyama T., Nishio Y., Kishimoto T., "Identification of alternative splicing FEBS Lett. 381:191-194(1996).
                                                                                                                                                                                                                                                                                                                          Fu X.-Y., Schindler C., Improta T., Aebersold R., Darnell J.E. J "The proteins of ISGF 3, the interferon alpha-induced transcript activator, define a gene family involved in signal transduction. Proc. Natl. Acad. Sci. U.S.A. 89:7840-7843(1992).
                                                                                                                                                                                                                                                                                                                                                                                                 Yan R., Qureshi S., Zhong Z., Wen Z., Darn "The genomic structure of the Statz."; coincident sites in Statl and Statz."; Nucleic Acids Res. 23:459-463(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                      Bluyssen H.A., Levy D.E.;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE=92366558; PubMed=1502204;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95192056; PubMed=7885841;
Yan R., Qureshi S., Zhong Z., Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                MEDLINE=97172544; PubMed=9020188;
                                                                                                                                                                                                                                                                                            MEDLINE=96176320; PubMed=8601453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    593 PGTFLLRFSES 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         603 PGTFLLRFSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            722
199
638
                                                                                                                                                                                                                                                                                                       SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human).
--azoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           722
199
638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85940
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Pred. No.
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                                                                                                                                                                                                                                                                       oto T., Akira
splicing for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 749
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uced transcriptional
l transduction.";
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      RA ICO Y., MIKAWA S., KODAYAShi E., Wada Y., Minezawa M.;
RI SUDMITTED (MAY-1997) to the EMBL/GenBank/DDBJ databases.

C. I-FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE IFN-STIMULATED CERSPONSE ELEMENT (ISRE) AND TO THE GAS ELEMENT. THIS MULTIPROTEIN TRANSCRIPTION FACTOR IS TERMED ISG3 (BY SIMILARITY).

C. I-SUBUNIT: IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STAT1-BETA, STAT2) OF ISG53, BECOME PHOSPHORYLATED ON TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX CONTROLLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (BY SIMILARITY).

C. I-SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN SUBCELLULAR INTO THE STATIANTY).

C. I-PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IFN-ALPHA (BY SIMILARITY): BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.

C. I-SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                     2_PIG
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                            STA2_PIG
002799;
                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999
15-JUL-1999
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; DNA Phosphorylation; SH2 domain; DOMAIN 572 667
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Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000980;
InterPro; IPR001217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIX:
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                       SIGNAL TRANSDUCER
                                                                                                                                                                                                                                  TISSUE=Muscle;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 GTFLLRFSESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604 GTFLLRFSESS
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$81491; AAB36226.1; -.
$81491; AAB36227.1; ALT_SEQ.
$42224; 1BF5.
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M97934; -; NOT_ANNO
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851
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(Rel.)
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STAT.
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100.0%;
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Last annotation updat
ACTIVATOR OF TRANSCRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY JAKS)
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSING (IN SHORT ISOFORM). E4C74674CB7A3215 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                          TRANSCRIPTION
                                                                                                                                                                                                                                                                                       Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                           864
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0.0079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 851;
                                                                                                                                                                                                                                                                                        SuS
                                                                                                                                                                                                                                                                                                   Euteleostomi;
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RESULT
STA2_MC
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Вb
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      A SUGIYAMA T., NISHIO Y., KISHIMOLO T., AKIRA S.;

RY "Identification of alternative splicing form of Stat2.";

REBS Lett. 381:191-194(1996).

C "IDENTIFICATION FACTOR THAT BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (ISRE) AND TO THE GAS ELEMENT. THIS MULTIPROTEIN TRANSCRIPTION FACTOR IS TERMED ISGF3.

C "IDENUAL": IN RESPONSE TO IFN ALPHA, BETA, THREE SUBUNITS (STAT1-C).

C ALPHA, STAT1-BETA, STAT2) OF ISGF3, BECOME PHOSPHORYLATED ON TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX CONTROLORY.

C TOGETHER WITH ISGF3 GAMMA (P48), A DAN-BINDING PROFEIN THAT SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (BY SIMILARITY).

C SIMILARITY).

C SIMILARIONE TO PHOSPHORYLATION (BY SIMILARITY).

C PRODUCED BY ALTERNATIVE SPLICING.

PRODUCED BY ALTERNATIVE SPLICING.

C ILTERN, KIDNEY, MUSCLE, AND THE BRAIN, LUNG, HEART, SPLEEN, LIVER, KIDNEY, MUSCLE, AND THE TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Transcription regulation; DNA-binding; Nuclear protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS: ANY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ish-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _MOUSE
STA2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and characterization of murine Stat2.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9WVL2; Q64189; Q64250; Q64188; 20-AUG-2001 (Rel. 40, Created)
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InterPro; IPR001217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB004061; BAA20332.1; ..
                                                                                                                                                                                                                                                                                                                                                        Paulson M.S., Mui A.,
"Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CD-
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation; SH2 domain.
DOMAIN 572 667
                                                                                                                                                                                                                                                                                             MEDLINE-96176320;
                                                                                                                                                                                                                                                                                                             SEQUENCE OF 595-658 FROM N.A.
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
PHOSPHORYLATED
                                                                                                                                                                                                                                                                                             PubMed-8601453;
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690
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                     Levy D.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 9;
Pred. No.
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                                                                                                                                                                                                                                                                                                             (ISOFORMS A AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi;
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RESPONSE
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0.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muridae;
TO
                                                                                                                                                                                                                                                                                                            B/C)
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IFN-ALPHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae;
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Matches 9
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InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00255; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF088862; AAD38329.1;
EMBL; S81342; AAB36228.2; -
EMBL; S81342; AAB36231.1; -
EMBL; S81342; AAB36230.1; I
EMBL; S81342; AAB36230.1; I
HSSP; P42224; 1BF5.
MGD; MGI:103039; Stat2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     P08159;
01-AUG-1988 (Rel. C
01-MAY-1991 (Rel. 1
15-DEC-1998 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
6-HYDROXY-D-NICOTINE OXIDASE (EC 1.5.3.6) (6-HDNO).
Arthrobacter oxidans.
Bacteria; Firmicutes; Actinobacteria; Actinobacteri
                                                                                                                                                                                                 Brandsch R., Hinkkanen A.E., Mauch L., Nagursky H., Decker K., "6-Hydroxy-D-nicotine oxidase of Arthrobacter oxidans. Gene str of the flavoenzyme and its relationship to 6-hydroxy-L-nicotine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
MUTAGENESIS OF HIS-71
MEDLINE-90033359; Pub
                                                                 Submitted
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=87304263; PubMed=3622516;
                                                                                                                                                                                                                                                                                                                                        Actinomycetales;
NCBI_TaxID=1671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARTOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation;
DOMAIN 571
                                                                                      Brandsch
                                                                                                                                                                                  oxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; DNA-binding;
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SIMILARITY: BELONGS T
SIMILARITY: CONTAINS
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PROSITE: Pout
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                    SEQUENCE FROM N.A.
STRAIN=S288C / FY73;
MEDLINE=97103776; Pubm
Purnelle B., Goffeau A
                                                                                                                                               P24720;
01-MAR-1992
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Lysine can replace arginine 67 in the mediation of covalent attachment of FAD to histidine 71 of 6-hydroxy-D-nicotine ox J. Biol. Chem. 265:12761-12762(1990)
-:- CATALYTIC ACTIVITY: (D)-6-HYDROXYNICOTINE + H(2)0 + O(2)
1-(6-HYDROXYPYRID-3-YL)-4-(METHYLAMINO)BUTAN-1-ONE + H(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mauch L., Bichler V., Brandsch R
"Lysine can renlact
                                                                                   MNEI OR MNE OR YOR350C OR 06353.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Site-directed mutagenesis
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Sen the Swiss Institute of Biol
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H->C, Y, S: NO FAD INCORPORAT
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Q24151; Q24181; Q9VDL8;
Q1-NOV-1997 (Rel. 35, C)
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Yeast 12:1475-1481(1996).
[2]
                                                MEDLINE=20196006; PubMed=10731132;
                                                                                STRAIN-BERKELEY;
                                                                                                                                                                                      Yan R., Small S., Desplan C., Dearolf C.R., Darnell J.E. Jr
"Identification of a Stat gene that functions in Drosophila
development ":
                                                                                                                                                                                                                                                      MEDLINE-96190809; PubMed-8608596;
                                                                                                                                                                                                                                                                                      TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                            Cell 84:411-419(1996)
                                                                                                                                                                                                                                                                                                                                                                                 Hou X.S., Melnick M.B., Perrimon N.;
"Marelle acts downstream of the Drosophila HOP/JAK kinase and encodes a protein similar to the mammalian STATs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
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3L; Z15258; CAA99678.1; -.
3L; X63112; CAA44826.1; -.
3; S19073; S19073.
3; S20175; S20175.
3; S0005877; MNE1.
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MRE4 gene encodes a novel protein kinase homologue
ic recombination in Saccharomyces cerevisiae.";
                                                                                                                                                     84:421-430(1996).
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Celniker S.E., Holt R.A., Ev
P.G., Scherer S.E., Li P.W.,
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  Evans C.A., Goc., Hoskins R.A.,
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3. 8.1;
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  Gocayne J.D.,
.A., Galle R.F.,
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RA Beeson K.Y., Bellows P.V., Berman B.P., Edyler, C., Brothkov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Downes M., Dugan-Roccha S., Dunkov B.C., Dunn P., RA Cherry C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ralush F., Kapren G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lian Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Murany D.M., Nelson D.L., RA Melson D.R., Nelson K.A., Siden K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Nahamer T., Siden K.A., Siden K., Sanders R.D.C., Scheeler F., Shen H., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Shen H., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Alliams S.M., Moydage T., Worley K.C., Wu D., Yang S., Yao Q. A., RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhao Q., Zheng L., Fer Signal T.R., Rubin G.M., Venter J.C., Sho Q., Zheng L., Frankus C., Frankus C., Frankus C., Frankus C., Stapleton M., Strong R., Sun E., Strong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., RA Zheng X.H., Weinstock G.M., Weinsto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I.
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin
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                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                 PUPAL, AND ADULT STAGES, WITH SOME DECREASE IN THE LATE EMBRYONIC STAGES. THE EXPRESSION IS UNIFORM IN UNFERTILIZED OR JUST FERTILIZED EGGS, SUGGESTING MATERNALLY DEPOSITED MRNA. AT BLASTODERM STAGE, EXPRESSION PATTERN SHOWS STRIPES, THAT ARE REMINISCENT OF MANY PAIR RULE GENES PATTERN.

PTM: TYROSINE PHOSPHORYLATED BY HOPSCOTCH. PHOSPHORYLATION IS
                                                                                                                                                                                                                                                                                                                               REQUIRED FOR DNA-BINDING ACTIVITY AND DIMERIZATION.
SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS
IN PARTICULAR TO MAMMALIAN STATS AND STAT6.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEMBER.
SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN RESPONSE TO PHOSPHORYLATION (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF THE PAIR RULE GENE EVEN-SKIPPED AT THE CELLULAR BLASTODERM STAGE, LEADING TO LARVAL SEGMENTATION DEFECTS.
SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT EMBRYONIC, LARVAL,
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Beunos P.V., Berman B.P., Bhandari D., Bolshakov S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lewis S.E.,
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Nelson C.R., Miklos G.L.G.,
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EMBL; U40070; AAC46984.1; EMBL; U46688; AAB02195.1; EMBL; AE003731; AAF55773.1 HSSP; P42224; 1BF5.

AAF55773.1;

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01-OCT-1996
20-AUG-2001
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VARSPLIC
CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                       "Cloning of
Stat5A and
                                                                                                                                                                                                                                                                                                                            Mol.
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ST5B_HU
P51692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0016917;
InterPro; IPR000980;
InterPro; IPR001217;
                                                                                                                                                 IFNgamma-mediated signaling.";
Cell 96:121-130(1999).
-!- FUNCTION: CARRIES OUT A DUAL
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Toloning of human
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                   Zhu M.-H., John S., Berg M., Leonard "Functional association of Nmi with s
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 Silva C.M., Lu H., Day R.N.; "Characterization and cloning of STAT5
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=96311205; PubMed=8732682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL TRANSDUCER
                                                                                                                                                                                                            PubMed=9989503
                                                                                                                                                                                                                                                                                         MEDLINE=96210005;
                                                                                                                                                                                                                                                                                                                                       activation by growth hormone
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                                                                                                                                                                                                                      INTERACTION WITH NMI.
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                                                                                                                                                                                                                                              Biol.
                                         SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH MILES OF SIMILARITY). INTERACTS WITH NMI. SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO RESPONSE TO PHOSPHORYLATION (BY SIMILARITY). FIN TYROSINE PHOSPHORYLATED (BY SIMILARITY). SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCR SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                           ACTIVATION OF TRANSCRIPTION. BINDS TACTIVATES PRL-INDUCED TRANSCRIPTION.
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                                                                                                                                                                                                                                              Chem.
                                                                                                                                                                                                                                          210005; PubMed-8631883;
Mietz 7., Modi W.S., John S., Leonard W.J.;
Mietz 7., Modi W.S., John S., Leonard W.J.;
f human Stat5B. Reconstitution of interleukin-2-induced
Stat5B DNA binding activity in COS-7 cells.";
hem. 271:10738-10744(1996).
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Conservative
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SH2.
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ACTIVATOR OF TRANSCRIPTION
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Institute.
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Pred. No.
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S -> T (IN REF. 2).
L -> H (IN REF. 2).
; BF3A622A29899161 CRC64;
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THE GAS
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are
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restrictions
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Best Local
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P42232; Q60804;
Q1-NOV-1995 (Rel. 32, C
Q1-NOV-1995 (Rel. 32, C
Q1-NOV-1995 (Rel. 32, C
Q1-AGG-2001 (Rel. 40, I
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STAT5B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                       Liu X., R "Cloning involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 604260;
             ÷
                                                                                                                           MEDLINE=96004632;
                                                                                                                                                                                                              STRAIN=C57BL/6 X A/J; TISSUE=Live
MEDLINE=95237198; PubMed=7720707;
                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                             Mus musculus
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DOMAIN 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
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                                                                                                                                     STRAIN-C57BL/6;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                              "Interleukin-3, granulocyte-macrophage colony stimulating factor
interleukin-5 transduce signals through two STAT5 homologs.";
MBO J. 14:1166-1175(1995).
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   613
                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 GTFLLRFS 611
                             X., Robinson G.W., Gouilleux F., Groner B., Hennighausen L.; oning and expression of Stat5 and an additional homologue (Stat olved in prolactin signal transduction in mouse mammary tissue. Ratl Acad. Sci. U.S.A. 92:8831-8835(1995).
FUNCTION: CARRIES OUT A DUAL FUNCTION: SIGNAL TRANSDUCTION AND ACTIVATION OF TRANSCRIPTION. BINDS TO THE GAS ELEMENT AND ACTIVATES PRL-INDUCED TRANSCRIPTION.
SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAM
           MEMBER (BY SIMILARITY)
SUBCELLULAR LOCATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   GTFLLRFS
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PF01017; STAT; 1.
1; SMC 252; SH2; 1.
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U47686; AAC50491.1;
P42224; 1BF5.
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8; Conservative
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  PHOSPHORYLATION
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Pfam; PF01017; STAT; 1.
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SMART; SM0252; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTICULARLY ABUNDANT IN MUSCLE TISSUE OF VIRGIN AND LACTATING FEMALES, AND OF MALES.
FEMALES, AND OF MALES.
DETECTED BOTH IN VIRGIN MOUSE AND AFTER MAMMARY GLAND INVOLUTION. THE LEVEL OF STAT5A INCREASES CONSTANTLY DURING PREGNANCY, BUT DECREASES DURING LACTATION.
TYROSINE PHOSPHORYLATED.
TYROSINE PHOSPHORYLATED.
SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.
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SEQUENCE
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DOMAIN 589 686 SH2.
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SUMMARIES

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2100 2100	AGATCATGGATGCGACCAACATCCTGGTGTCTCCACTTGTCTACCTCTACCCCGACATTC	2041	Оу
2040	AGCCATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGGCTATA 	1981 1981	ОУ
1980 1980	GGGTCACTTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTA-3	9 9	р ₆ Оу
1920 1920	TAAGCACAAAGCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAAGAAGGAG 	98	ОУ
1860 1860	CCCTTTGGAATGAAGGGTACATCATGGGTTTCATCAGCAAGGAGCGGGAGCGGGCCATCC	80	DЬ
1800	TTCTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTGG 	1741 1741	Оy
1740 1740	ACTACTCAGGGTGTCAGATCACATGGGCTAAATTCTGCAAAGAAAACATGGCTGGC	1681 1681	Qу
1680 1680	GAGGGCTGAGCATCGAGCAGCTGACAACGCTGGCTGAGAAGCTCCTAGGGCCTGGTGTGA	1621 1621	Оу
1620 1620	TTGGAACCTGGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCACCAACCA	1561 1561	Оy
1560 1560	TGTGGTATAACATGCTGACCAATAACCCCAAGAACGTGAACTTCTCACTAAGCCGCCAA	1501 1501	рь
1500 1500	CCTTGCCAGTTGTGGTGATCTCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATCC	1441 1441	Оy
1440 1440	TGATCACCTTCGAGACTGAGGTGTACCACCAAGACCCAAGATTGACCTAGAGACCCACT	1381 1381	Qу
1380 1380	GTGGGAATGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCACC	w w	Оy
1320 1320	AGTCTAACAACGGCAGCCTGTCTGCAGAGTTCAAGCACCTGACCCTTAGGGAGCAGAGAT 	126: 126:	Dp Qy
1260 1260	TCAGAGGGTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGG 	NN	Оу
1200 1200	TGAATTATCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCC	1141	Qy Db
1140 1140	TCATCAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGT	1081	Qу
1080	AGAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCCGGACCGGCCCTTAG	1021 1021	Qy Db

REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE

Unknown.

M Unknown.

Unclassified.

1 (bases 1 to 2869)

Karras, J.G.

Antisense modulation of stat3 expression

Location/Qualifiers

1. 2869

vorganism="unknown"

755 a 743 c 772 g 599 t

BASE COUNT ORIGIN

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01	2869 bp DNA PAT 16-MAY-2001 2 from patent US 6159694.	AR121061 Sequence 8	מ ביים	DEFI
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	CAGGAGGTTCCTCTTTAAAATTAAAAAAAAAAAAAAAAA	TAGGACTAAGCC	2821	Ф
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2820	ACCCCATTCTGGGAACTCCTGGCTCTGCACTTTCAACCTTGCTAATATCCACATAGAAGC 28	ACCCCATTCTGG	2761	Db
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2760	TGCCCATGGCTACCTGTTGCCCCACTCTGTGAGCTGAT 27	TTGTTAGACAAG	2701	DЬ
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2640	2	TGTTATGTAAAG	2581	DЬ
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2580	ATCTTTGGGCATCTGGGCACTTTTAAAAGAGAGAATGAGTGAG	ATCTTTGGGCAA	2521	Д
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2520	TCGTCTGAAACTCCTAACTTTGTGGTTCCAGATTTTTTTT	TCGTCTGAAACT	2461	DЬ
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2340	GAAATAACGGTGAAGGTGCTGAGCCCTCAGCAGGAGGGCAGTTTGAGTCGCTCACGTTTG 23	GAAATAACGGTG	2281	DЬ
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Query M Best Lo Matches Oy 1 Db 1	atch 29.8%; Score 2864.2; DB 6; Length 2869; cal Similarity 99.9%; Pred. No. 0; 2866; Conservative 0; Mismatches 3; Indels 0; Gap GCCGCGACCAGCCAGGCCAGTCGGGCTCAGCCCGGAGACAGTCGAGACCCCTGACT 6 [0 0 s
Qy 12 Db 12	1 TGCACCAGCTGTACAGCGACACGTTCCCCCATGGAGCTGCGGCAGTTCCTGGCACCTTGGA 1:	80
Qy 18 Db 18	1 TTGAGAGTCAAGACTGGGCATATGCAGCCAGCAAAGAGTCACATGCCACGTTGGTGTTTC 2	40
Qy 24 Db 24	1 ATAATCTCTTGGGTGAAATTGACCAGCAATATAGCCGATTCCTGCAAGAGTCCAATGTCC 3	00
Qy 30 Db 30	1 TCTATCAGCACAACCTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGC 3	60
Oy 36	1 CAATGGAAATTGCCCGGATCGTGGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCTCCAGA 4	20
Qy 42 Db 42	1 CGGCAGCCACGGCAGCCAGCAAGGGGGCCAGGCCAACCCCAACAGCGCCGC	80
Qy 48 Db 48	1 CAGAGAAAGCAGCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGCG	40
Qy 54 Db 54	1 TAGAACAGAAAATGAAGGTGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAA 6	00
Qy 60 Db 60	1 CCCTCAAGAGCCAAGGAGACATGCAGGATCTGAATGGAAACAACCAGTCTGTGACCAGAC 6	60
Qy 66 Db 66	1 AGAAGATGCAGCAGCTGGAACAGATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTG 7	20
Qy 72 Db 72	1 TGAGTGAGCTGGCGGGGCTCTTGTCAGCAATGGAGTACGTGCAGAAGAACACTGACTG	80
Qy 78 Db 78	1 AAGAGCTGGCTGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACA 8	40
Qy 84 Db 84	1 TCTGCCTGGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCC 9	00
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Zhong, Z.,
Stat3 and
                               1 (bases 1 to 2869)
2hong, Z., Wen, Z. and Darnell, J.E.
stat3: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6 Science 264, 95-98 (1994)
94188718
                                                                                                Mus musculus
Eukaryota, Metazoa;
Mammalia; Eutheria;
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Mus musculus signal transducer and
(Stat3) mRNA, complete cds.
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Wen, Z. and Darnell, J. Stat4: members of the
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Submitted (18-FEB-1994) 2. Zhong, The Rockefeller University,
Molecular Cell Biology Laboratory, 1230 York Avenue, New York,
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RIVARCLWEESRLLQTAATAAQQGGQANHPTAAVYTEKQOMLEQHLQDVRKYQDLEQ
KMKVVENLQDDEPPNYKTLKSGGDMQDLMGNNGSYTQKWQQLEQMLTALDQMRRSIV
SELAGLLSAMEYVQKTLTDEELADWKRRQQIAQIGGPPNICLDBLENWITSLAESQLQ
TRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELKSAFVVERQCMMHPD
TPQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELKASAFVVERQCMPMHPD
RPLYIKTQQQFTSYKRLLVKFPELNYQLKIKVCJDKDSGDVAALRSGRKENILGTWYK
VMNMEESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQGL
KIDLETHSLPVVVISNICQMPNAMASILWYNMLTWNPKNVNFTTKPPIGTWQVAEVL
SWQFSSTTKRGLISIEQLTTLAEKLLGPGVYSGCQITHWAKFCKEMMAGKGFSHVWHLD
NIIDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWV
EKDISCKTQIGSVEPYTKQQLNNNSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEA
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/citation=[1]
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69. .2381
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/clone_lib="Mouse thymus
/dev_stage="6-8 weeks"
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/protein_id="AAA19452.1"
/db_xref="GI:458706"
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/db_xref="taxon:10090"
/sex="female"
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1380 1380	GTGGGAATGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCACC	1321 1321
1320 1320	AGTCTAACAACGGCAGCCTGTCTGCAGAGATTCAAGCACCTGACCCTTAGGGAGCAGAGAT	1261 1261
1260 1260	TCAGAGGGTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGG 	2 2
1200 1200	TGAATTATCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCC	
1140 1140	TCATCAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGT	
1080	AGAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCCGGACCGGCCCTTAG	1021 1021
1020 1020	TCGTGCAGCACCGCCCCATGCTGGAGGAGGAGGATCGTGGAGCTGTTCAGAAACTTAATGA	96 <u>1</u>
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900	TCTGCCTGGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCC 	
840 840	AAGAGCTGGCTGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACA	
780 780	TGAGTGAGCTGGCGGGGCTCTTGTCAGCAATGGAGTACGTGCAGAAGACACTGACTG	721 721
720 720	AGAAGATGCAGCAGCTGGAACAGATGCTCACAGGCCTGGACCAGATGCGGAGAACCATTG	
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540 540	CAGAGAAGCAGCAGCATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATC	481
480 480	CGGCAGCCACGGCAGCCAGCAAGGGGGGCCAACCACCACC	
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2461 TCGTCTGAAACTCCTAACTTTGTGGTTCCAGATTTTTTTT	Qy Db
2401 GCAGAGACGTGACTTGAGACACCTGCCCCGTGCTCCACCCCTAAGCAGCC	Qy Db
2341 ACATGGATCTGACCTCGGAGTGTGCTACCTCCCCCATGTGAGGAGCTGAAA	Qy Db
Y 2281 GAAATAACGGTGAAGGTGCTGAGCCCTCAGCAGGAGGGCAGTTTGAGTCGCT	Qy Db
Y 2221 GCAGCAATACCATTGACCTGCCGATGTCCCCCGCGCACTTTAGATTCATTGAT	Qy Db
/ 2161 ACCCAGGTAGTGCTGCCCCGTACCTGAAGACCAAGTTCATCTGTGTGACAC 	Qy Db
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7 1981 AGCCATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCAT	Qy Db
1921 GGGTCACTTTCACTTGGGTGGAAAAGGACATCAGTGGCAAG/ 	Qy Db
7 1861 TAAGCACAAAGCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAA 	Db Db
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/ 1621 GAGGGCTGAGCATCGAGCAGCTGACAACGCTGGCTGAGAAGCTCCTAGGGCC 	Qy Db
7 1561 TTGGAACCTGGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCAC 	Qy Db
1501 TGTGGTATAACATGCTGACCAATAACCCCAAGAACGTGAACTTCTTCACTAAGG	Qy Db
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TCTATCAGCACAACCTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGC
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Sequence
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Bromberg, J.F., Wrzeszczynska, M.H., Zhao, Y. and Darnell, J.E. Jr Constitutively active transcription factors and their uses for identifying modulators of activity including dysproliferative cellular changes
Patent: US 6235873-A 9 22-MAY-2001;
                                                                                                                                                                                                                                                                                                                                      Unknown
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TGATCACCTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACT
                       TCAGAGGGTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGG
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ye	ontact: (Dickson, Mark) mcd@paxil.stanford.edu ickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and . M.			
Genome CA 94305	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) nequencing by: Sequencing Group at the Stanford Human sr, Stanford University School of Medicine, Stanford, http://www-shgc.stanford.edu			
	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. CNAA Library Propagation: Life Technologies, Inc	COMMENT	COM	
	<pre>USA NIH-MGC Project URL: http://mgc.nci.nih.gov</pre>	REMARK	7 2	
alian cer 2590,	Direct Submission Submitted (28-FEB-2001) National Institutes of Health, Mammali Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-259	JOURNAL	ų i	
	2964)	AUTHORS	REF	
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1011 3,	clone MGC:6089 IMA	INTITION	200	
	BC003806 2964 bp mRNA ROD 12-J	RESULT 6 BC003806 LOCUS	RESI BC01 LOCI	
	TAGGACTAAGCCCAGGAGGTTCCTCTTTAAATTAAAAAAAA	2821	DЬ	
	TAGGACTAAGCCCAGGAGGTTCCTCTTTAAATTAAAAAAAA	2821	Qy	
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2640		2581	Db	
2640	TGTTATGTAAAGAGGAGAGACCTCTGAGTCTGGGGATGGGGCTGAGAGCCAGAAGGGAGGC	581	οy	
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2580	ATCTTTGGGCAATCTGGGCACTTTTTAAAAAGAGAGAAATGAGTGAG	2521	Ş	

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96278730
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3 (bases 1 to 2924)
Caldenhoven, E., van Dijk, T.B., Solari, R., Armstron Raaijmakers, J.A.M., Lammers, J. W.J., Koenderman, L. STAT3beta, a splice variant of transcription factodominant negative regulator of transcription J. Biol. Chem. 271 (22), 13221-13227 (1996)
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Schaefer, T.S. Sanders, L.K. and
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Schaefer, T.S., Sanders, L.K.
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Eutheria; Rodentia;
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1210 1314	1151 GCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCCTCAGAGGGTC 	Qу
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G 2290	TGTC	2231	Qy
- 2316		N	Db
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3 2274	GGCATTTGGAAAGTACTGTAGGCCCGAGAGCCAGGAGCCCCGAAGCCGACCCAGGTAG	Ń	₽ ,
3 2170	ATTTGGAAAGTACTGTAGGCCCGAGAGCCAGGAGCACCCCGAAGCCGACCCAGGT	2111	γo
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A 2110	GCGACCAACATCCTGGTGTCTCCACTTGTCTACCTCTACCCCGACATTCCCAAGGAGG	2051	Qγ
A 2154	ര -	2095	Db
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1854			₽ .
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Mus musculus
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University School of Medicine, 550
10016, USA
                                                                                                                                                                                                                    Acute phase response factor and additional members of the interferon-stimulated gene factor 3 family integrate diversignals from cytokines, interferons, and growth factors J. Biol. Chem. 269, 24391-24395 (1994)
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 2924)
Raz,R., Durbin,J.E. and Levy, [
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KMKVVENLQDEDENYKTLKSQGDMQDLUGNUQSVTROWMQQLEQMLTSLAESQLQ
TRQQIKKLEELQQXVSYKGDDJYQHFPWLEERIYGLERRLMKSAFVVERQOCHTMTK
TRQQIKKLEELQQXVSYKGDDJYQHFPWLEERIYGLERRLMKSAFVVERQOCHTMTK
VMNMEESNUGSLSAEFKHLTJREDGRCGNGGRANCDASIIVTEELHLITFETEVYHQGL
KIDLEFHSLPVVTISNICQMPNAWASILWYNMLTNNPKNVNFFTKPDIGTWDOVAEVI.
SWQFSSTTKRGLISIBQLTTLAEKLLGFQVNYSGCQITWAKFCKENMAGKGFSFWWHLD
NIIDLYKKYILALMNEGYIMGFISKERFARILSTKPGTFLLRFSESKEGGVTFTWV
EKDISGXTQIGSVEPYTYQQLUNNNSFAEIIMGYXIMDATNILVSBLYYLVEDIFKEEA
FGKYCRPESQDHPEADPGAAPYLKTKFICVTFTTCSNTIDLPMSPRTLDSLMQFGNNG
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1807 1885	8 CTTCTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTGGCCCTTTG	Qy 174 Db 182	
1747 1825	8 AGGGTGTCAGATCACATGGGCTAAATTCTGCAAAGAAAACATGGCTGGC		
1687 1765	8 GAGCATCGAGCAGCTGACAACGCTGGCTGAGAAAGCTCCTAGGGCCTGGTGTGAGCTACTC	Qy 162 Db 170	
1627 1705	8 CTGGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCACCAACCA	Qy 156 Db 164	
1567 1645	8 TAACATGCTGACCAATAACCCCAAGAACGTGAACTTCTCACTAAGCCGCCAATTGGAAC		
1507 1585	8 AGTTGTGGTGATCTCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATCCTGTGGTA 		
1447 1525	8 CTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACTCCTTGCC	Qy 138 Db 146	
1387 1465	8 TGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCACCTGATCAC	Qy 132 Db 140	
1327 1405	8 CAACGGCAGCCTGTCTGCAGAGTTCAAGCACCTGACCCTTAGGGAGCAGAGATGTGGGAA	Qy 126 Db 134	
1267 1345	8 GTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGGAGTCTAA 	8	
1207 1285	8 TCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCCTCAGAGG 	Oy 114 Db 122	
1147 1225	8 GACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGTTGAATTA	Qy 108 Db 116	
1087 1165	8 CTTCGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCGGACCGGCCCTTAGTCAA	Oy 102 Db 110	
1027 1105	8 GCACCGGCCCATGCTGGAGGAGAGAGTCGTGGAGCTGTTCAGAAACTTAATGAAGAGTGC	Oy 96 Db 104	
967 1045	8 AATTAAGAAACTGGAGGAGCTGCAGCAGAAAGTGTCCTACAAGGGCGACCCTATCGTGCA (QY 90	
907 985	8 GGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCCGCCAACA (Qy 84. Db 92	
847 925	8 GGCTGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACATCTGCCT 8	Qy 781 Db 861	
	GCTGGCGGGGCTCTTGTCAGCAATGGAGTACGTGCAGAAGACACTGACTG	Qy 728 Db 806	

	TAAGCCCA-GAGGTTCCTCTTTAAAT	2898	Db
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2897	AACCTTGCTAATATCCACATAGAAGCTAG	2839	Db
2825	TTCTGGGAACTCCTGGCTCTGCACTTTCAACCTTGCTAATATCCACATAGAAGCTAGG	2766	Qy
2838	AAGTGCCTCCTGGTGCCCAT-GCATCCTGTTGCCCCACTCTGTGAGCTGATACC	2780	Db
2765	GACAAGTGCC	2706	Qy
2779	CAGCTC-GGGGTTGGTTGT	2721	Дb
2705	GAACACCTCCTGTCCTGCCCGCCTGCCTTTTTTCAGCAGCTC	2646	Qy
2720	AGGAGAGCACCTCTGAGTCTGGGGATGGGGCTGAGAGCAGAAGGGAGCAAG	2663	Db
2645	TAAAGAGGAGAG-ACCTCTGAGTCTGGGGGATGGGGCTGAGAGGAAGGGAAG	2587	Qy
2662	GGCACTTTTTAAAATAGAGAAATGAGTGAGTGTGGGTGATAAACTGTTA	2603	Db
2586	GGCAATCTGGGCACTTTTAAAA	2527	Qy
2602	AACTCCTAACTTTGTGGTTCCAGATTTTTTTTTTTTTAATTTCCTACTTCTGCTATCTT	2543	Db
2526	AAACTCCTAACTTTGTGGTTCCAGA-TTTTTTTTTTAATTTCCTACTTCTGCTATCTTT	2468	Оу
2542	GACTTGAGACACCTGCCCCGTGCTCCACCCCTAAGCAGCCGAACCCCCATATCGTCTG	2483	Db
2467	GTGACTTGAGACACCTGCCCCGTGCTCCACCCCTAAGCAGCCGAACCCCCATATCGTCTG	2408	Оу
2482	CTCCCCCATGTGAGGAGCTGAAACCAGAAGCTGCAGAGA	2423	Дb
2407	GACCTCGGAGTGTGCTACCTCCCCCCATGTGAGGAGCTGAAACCAGAAGCTGCAGAGA	2348	Qy
2422	TGAAGGTGCTGAGCCTCAGCAGGAGGGCAGTTTGAGTCGCTCACGTTTGACATGGA	2363	Db
2347	GGTGAAGGTGCTGAGCCCTCAGCAGGAGGGCAGTTTGAGTCGCTCACGTTTGACATGGA	2288	Оу
2362	TAGATTCATTGATGCAGTTTGGAAATAA	2303	ДD
2287	ACCATTGACCTGCCGATGTCCCCCCCGCACTTTAGATTCATTGATGCAGTTTTGGAAATAA	2228	Qy
2302	ACCAACGACCTGCAGCAA	2245	DЪ
2227	TGCTGCCCCGTACCTGAAGACCAAGTTCATCTGTGTGACACCAACGACCTGCAGCAA	2168	Qy
2244	CCGACCCAG-	2186	Db
2167	GAGGCATTTGGAAAGTACTGTAGGCCCGAGAGCCAAGGAGCACCCCGAAGCCGACCCAGG	2108	у
2185	CCCAAGGA	2126	Db
2107	GATGCGACCAACATCCTGGTGTCTCCCACTTGTCTACCTCTACCCCGACATTCCCAAGGA	2048	Ογ
2125	CTATAAGATCAT	2066	Db
2047	ACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGGCTATAAGATCAT	1988	Qy
2065	ATCCAGTCTGTAGAGCCATA	2006	Db
1987	TTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTAGAGCCATA	1928	Оу
2005	GGTCAC	1946	Db
1927	AAGCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAAGAAGGAAG	1868	Оу
1945	GGGCCATCCTAAGCAC	1886	Db
1867	AATGAAGGGTACATCATGGGTTTCATCAGCAAGGAGCGGGAGCGGGCCCATCCTAAGCAC	1808	Qy

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GCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCCAGGATCTAGAACAGAA 550
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                                                                                                                                  AGACTGGGCATATGCAGCCAGCAAGAGGTCACATGCCACGTTGGTGTTTCATAATCTCTT
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Unknown.
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Patent: US 5719042-A 7 17-FEB-1998;
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Sequence 7 from patent
188783
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Kishimoto, T. and Akira, S.
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1810	CTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTGGCCCCTTTGGAA :	1751	Qy
2000		1941	Db
1750 1940	GTGTCAGATCACATGGGCTAAATTCTGCAAAGAAAACATGGCTGGC	1691 1881	Оу
1690 1880	CATCGAGCAGCTGACAACGCTGGCTGAGAAGCTCCTAGGGCCTGGTGTGAACTACTCAGG	80 0	Qy Db
1630	GGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCACCAACCA	1571	Qy
1820		1761	Db
1570 1760	CATGCTGACCAATAACCCCAAGAACGTGAACTTCTTCACTAAGCCGCCAATTGGAACCTG	7 5	Qy Db
1510	TGTGGTGATCTCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATCCTGTGGTATAA	1451	Qy
1700 .		1641	Db
1450 1640	CGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACTCCTTGCCAGT	υniω	Qy Db
1390 1580	AGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCACCTGATCACCTT		Qy Db
1330	CGGCAGCCTGTCTGCAGAGTTCAAGCACCTGACCCTTAGGGAGCAGAGATGTGGGAATGG	1271	Qy
1520		1461	Db
1270 1460	TCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGGAGTCTAACAA	4 2	Qy Db
1210	GCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCCTCAGAGGGTC	w ju	Qy
1400			Db
1150	TGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGTTGAATTATCA	1091	Qy
1340		1281	Db
1090 1280	CGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCGGGACCGGCCCTTAGTCATCAAGAC	20	Qy Db
1030	CCGGCCCATGCTGGAGGAGAGGATCGTGGAGCTGTTCAGAAACTTAATGAAGAGTGCCTT	971	Qy
1220		1161	Db
970	<i>p p</i>	911	Qy
1160		1101	Db
910	CCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCCGCCAACAAT	851	Qy
1100		1041	Db
850	TGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACATCTGCCTGGA	791	Qy
1040		981	Db
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CAGGCCGGCCAGTCGGGC--TCAGCCCGGAGACAGTCGAGACCCCTGACTGCAGCAGGAT
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Patent: US 5719042-A 8 17-FEB-1998;
Location/Qualifiers
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Kishimoto, T. and Akira
Nucleic acids encoding
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                                       GGCATTTGGAAAGTACTGTAGGCCCGAGAGCCAGGAGCACCCCGAAGCCGAACCCAGGTAG
                                                              TGCGACCAACATCCTGGTGTCTCCACTTGTCTACCCTCTACCCCGACATTCCCAAGGAGGA
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Akira,S., Nishio,Y., Inoue,M., Wang,X.-J., Shi,W., Matsusaka,T., Yoshida,K., Sudo,T., Naruto,M. and Kishimoto,T.
Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling pathway cell 77, 63-71 (1994)
94208062
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/product-*acute phase response factor*
/product-*acute phase response factor*
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SELAGLLSAMEYVOKTITDEELADMKRROQIAGIGGPPNICLORLENMTTSLAESQLQ
XEMACYVENLQDDPFNYKTLKSQCDMQLLGNNGSTTROKNQQLEOMLTALDQMR8SIV
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TRQQIKKLEELQQKVSYKGDPIVOHPMLEERIVELFRUMKSAFVVEROPCMPMHPD
RPLYKTGVQOFTKVRLLVKFPELNYQLKIKVCIDDSCDVAALRSGRKNILGTMYK
VINMEESNNGSLSAEFKHLTLREORCGNGGRANCDASLIVTEELHLITFETEVYHQGL
KIDLETHSLPVVVISNICQMPNAMASILMYNMLTNNPKNVNFFTRAPIGTWDVAEVL
SWOFSSTTKRGLISIEQLTTLAEKLLGPGVNYSGCQITTWAKFCKENMAGKGFFFFWWLD
NIIDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRESESKEGGVTFTWV
EKDISGKTOJOSVEPTTROQLNNMSFAEIIMGYKIMDATNILVSPLVYLYDDIFKEA
FGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSNTIDLPMSPRTLDSLMQFGNN
GEGAEDSAGGODESLTFONDLTSBCATSBM*
83 a 706 c 748 g 515 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sub_species="domesticus"
/db_xref="taxon:10090"
/tissue_type="liver"
/tissue_lib="lambda gtll cl
259 2571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="APRF"
259. .2571
/gene="APRF"
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Quer Best	y Ma Loc hes	tch 84.2%; Score 2415.6; DB 10; Length 2652; al Similarity 99.3%; Pred. No. 0; 2436; Conservative 0; Mismatches 14; Indels 2; Gaps	<u></u>
Qу	13 201	CAGGCCGGCCAGTCGGGCTCAGCCCGGAGACAGTCGAGACCCCTGACTGCAGCAGGAT 70	
Qy	71	GCTCAGTGGAACCAGCTGCAGCAGCTGGACGCACCTGCAGCTGCACCAGCT 13	
Db	1	TCAGTGGAACCAGCTGCAGCAGCTGGACACGCTACCTGGAGCAGCTGCACCAGCT 3	
Qy	w	GTACAGCGACACGTTCCCCATGGAGCTGCGGCAGTTCCTGGCACCTTTGGATTGAGAGTCA 190	
<u></u>	o K	TACAGCGACAGCIICCCCAIGGAAAGAGTCACATGCCACGTTGGTGTTTCATAATCTCTT 25	
99 99	191 381	μ. U	
Qγ	251	GGTGAAATTGACCAGCAATATAGCCGATTCCTGCAAGAGTCCAATGTCCTCTATCAGC	
Db	441	GGGTGAAATTGACCAGCAATATAGCCGATTCCTGCAAGAGTCCAATGTCCTCTATCAGCA 500	
Qy	311	CAACCTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGCCAATGGAAAT 370	
DЬ	501	AACCTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGCCAATGG	
Qy	371		
DЬ	561	GCCCGGATCGTGGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCTCCAGACGGCAAGACGC	
P 09	431	GGCAGCCCAGCAAGGGGGCCAAGCCAACCACCCAACAGCCGCC	
ρ _γ	9	TGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATCTAGAACAG	
Db	681	GCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATCTAGAACAGAA 740	
Оу	551	- \$	
Db	741	TGAAGGTGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAACCCTCAAGAG 8	
Оу	611	7	
рb		CAAGGAGACATGCAGGATCTGAATGGAAACCAACCAGTCTGTGACCAGACAGA	
Qy	671	GCAGCTGGAACAGATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTGTGAGTGA	
	7 0	COCOCCETTTTCTCACCAATGGAGTACCTCCAGAAGACACTGACTGA	
Db *5		GCCGGGGCTCTTGTCAGCAATGGAGTACGTGCAGAAGACACTGACTG	
Оу	791	GACTGGAAGAGGCGGCC	
Db	981	TGGAAGAGGCGGCAGCAGATCGCGTGCATCGGAGGCCCTCCCAACATCTGCCTGG	0
Qy	851	CCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCCCGCCAACAAAT 910	
DЪ	1041	CGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCCGCCAACAAAT 1	ō
Qy	911	TAAGAAACTGGAGGAGCTGCAGCAGAAAGTGTCCTACAAGGGCGACCCTATCGTGCAGCA 970	
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i Shinriyou S., Kishimoto C.;
I "TRANSCRIPT APRF";
Patent number JP1995324096-A/2, 1;
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Eukaryota;
Eutheria; R
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12-DEC-1995
03-APR-1995 JP 1995077584
04-APR-1994 JP 94P 65825
SHINRIYOU SHIZUO, KISHIMOTO CHUZO
CO7K14/52, A61K31/70, A61K38/00, A61K39/395, A61K48/00, C07H21/04,
C12R1:19),
C12R1:19),
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Rodentia;
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 Location/Qualifiers
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/organism="Mus sp."
/tissue_type="liver"
/59. .2571
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Sciurognathi; Muridae;
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                                                Location/Qualifiers
             /product="APRF"
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/db_xref="taxon:10095"
/organism="Mus sp."
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Pred. No. 0;
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Ripperger, J.A.
Direct Submission
Submitted (26-SEP-1995) J.A. Ri
Erlangen-Nuernberg, Lehrstuhl f
Erlangen, FRG
                                                                                                                                                                                                                                                                                                                                                                       R.ncrvegicus mRNA 1
X916.0
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J. Biol. Chem. 270
96102059
2 (bases 1 to 2924
                                                                                                                                                                                                                                                                                                                 stat3 gene; stat3 protein.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                Ripperger, J.A., Fritz, Fey, G.H.
Transcription factors
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/gene="Stat3"
/notce="single, polypeptid
heterodimers for specific
/codon_start=1
/product="Stat3 protein"
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                                                          /gene="Stat3"
                                                                                 /tissue_type="liver, acute phase"
/cell_type="predominantly hepatocytes"
/clone_lib="lambda ZapII (Stratagene)"
                                                                                                                       /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                     Location/Qualifiers
                                                                                                              /dev_stage="adult"
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or specific DNA-binding"
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L f. Genetik, Staudtstra
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CTGGCAGGGCTCTTGTCAGCAATGGAGTACGTGCAGAAGACACTGACCGATGAAGAGCTG
                AAAATGAAGGTGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAACCCTCAAG
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EKDISCKTQIOSVEPYTRQQLNNMSFAEIMGYKIMDATNILVSPLVYLYPDIPKEEA
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1532	73 GTGGGAATGGGGGCCGAGCCAATTGTGATGCTTCCCTGATTGTGACTGAGGAGCTGCACC	b 14	
1380	1 GTGGGAATGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCAC	0у 13:	
1472	CAGCCTCTCTGCAGAATTCAAACACTTGACCCTGAGGGAGCAGAGA	14	
1320	1 AGTCTAACAACGGC	Qy 12	
1260	01 TCAGAGGGTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGG 	Qу 12 рь 13	
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1292	AAGACCGGCGTCCAGTTCACTACTAAAGTCAGGTTGCTGGTCAAGTTCCCTGAG	N	
-	81 TCATCAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGT	Qy 101	
1232	73 AAAGTGCCTTTGTGGTGGAGCGGCAGCCCTGCATGCCATGCATCCTGACCGGCCCCTCG	Db 117	
1080	1 AGAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCCGGACCGGCCCTT	Oy 10:	
1172	3 TTGTACAGCACCGGCCGATGCTGGAGGAGAGGATCGTGGAGCTGTTCAGAAACTTAATGA	Db 111	
1020	1 TCGTGCAGCACCGGCCCATGCTGGAGGAGAGGATCGTGGAGCTGTTCAGAAACTTAATGA	Qу 96	
1112	3 GTCAACAAATTAAGAAACTGGAGGAGTTGCACCAAAAAGTTTCCTACAAAGGGGACCCCA	Db 105	
960	1 GCCAACAAATTAAGAAACTGGAGGAGGCGGCAGCAGAAAGTGTCCTACAAGGGCGACCCTA	Qу 90	
1052	3 TCTGCCTAGATCGGCTAGAAAACTGGATAACGTCATTAGCAGAATCTCAACTTCAGACC	Db 99	
900	1 TCTGCCTGGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAAACTTCAGACCC	Оу 84	
992	3 AGGAGCTGGCTGACTGGAAGAGGCGGCAACAGATTGCCTGCATTGGAGGCCCGACCAACA	ر و	
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720	1 AGAAGATGCAGCAGCTGGAACAGATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTG	Оу 66	
812	3 CCCTCAAGAGTCAAGGAGACATGCAAGATCTGAATGGAAACAACCAGTCAGT	Db 75	
660	1 CCCTCAAGAGCCAAGGAGACATGCAGGATCTGAATGGAAACAACCAGTCTGTGACCAGAC	Оу 60	
752	3 TAGAACAGAAAATGAAAGTGGTAGAGAATCTCCAGGATGACTTTGATTTCAACTATAAAA	Db 69	
600	AGAACAGAAAATGAAGGTGGTGGAGAAACCTCCAGGACGACTTTGATTTCAACTACAAAA	Qy 54	
692	TGCAGGATC	Db 63	
540	AGAGAAGCAGCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCCAGGATC	Оу 48	
632	TGA	Db 57	
	GGCAGCCACGGCAGCCAGCCAAGGGGGGCCAGGCCAACCACC		_
572	1 CAATGGAAATTGCCCGGATCGTGGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCTCCAGA 4	Qy 36 Db 51	
, ,	CTATCAGCACAATCTACGAAGAATCAAGCAGTTTCTTCAGAGCAGGTATCTTGAGAAGC		_
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- Ş 2577 AAACTGTTATGTAAA 2591 || || || || || || 2730 CTGCTTTATCTAAA 2744
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Search completed: March 19, 2002, 15:17:28 Job time: 4591 sec

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ALIGNMENTS

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AAQ89340 standard;

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AAQ89340;

27-SEP-1995

(first entry)

Mouse Stat3 (19sf6) cDNA.

24-SEP-1993; 24-SEP-1993; 11-MAR-1994; 11-MAR-1994; (UYRQ) UNIV Key Signal transducer and activator of transcription; Stat3; receptor recognition factor; transcription cellular debilitation; derangement; dysfunction; interferon-gamma; ss. 26-SEP-1994; 30-MAR-1995 WO9508629-A. Mus sp. ROCKEFELLER. 93US-0126588. 93US-0126595. 94US-0212184. 94US-0212185. 94WO-US10849 Location/Qualifiers 69..2381 /*tag= a STAT; 19sf6; factor;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays a for treating ceilular debilitations, derangements and/or
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Best L
                                                                                                                                    Matches
                                                                                                                                                                                                           Mouse cDNA clone 19sf6 (AAT31280) codes for mouse signal transducer and activator of transcription (STAT) protein STAT4 (AAW03180), a protein that serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription. STAT4 includes a DNA-binding domain (see also AAW03167) useful for screening for antagonists that modulate STAT activity. The cDNA, which was obtd. from splenic/thymic cells, can be used for prodn. of STAT4 or mutant STAT4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1280
                                                                                                                                                                                                                                                                                                                                             New STAT protein DNA-binding domain peptide(s) - useful idiagnosing, preventing or treating cellular dysfunction, oncogenesis, inflammation, parasitic disease or autoimmun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                         Sequence 2869 BP;
                                                                                                                                                                                                                                                                                                                         Disclosure; Page 93-96; 138pp;
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DNA binding
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          TGCACCAGCTGTACAGCGACACGTTCCCCATGGAGCTGCGGCAGTTCCTGGCACCTTGGA
                                                    GCAGCAGGATGGCTCAGTGGAACCAGCTGCAGCAGGTGGACACACGCTACCTGAAGCAGC
                                          gcagcaggatggctcagtggaaccagctgcagcagctggacacacgctacctgaagcagc
                                                                                     gccgcgaccagccaggccagtcgggctcagcccggagacagtcgagacccctgact
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tgcaccagctgtacagcgacacgttccccatggagctgcggcagttcctggcaccttgga
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gaaata	2341	Q E	1260	tcagagggtctcgggaaatttaacattctgggcacgaacacaaaagtgatgaacatggagg	Db 1201
- A	2281	Qy	1260	TCAGAGGGTCTCGGAAATTTAACATTCTGGGCACGAACACACAAAAGTGATGAACATGGAGG	Оу 1201
gcagca	2221	Db	1200	TGAATTATCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCC	Qy 1141 Db 1141
	2161	O D !	1140	TCATCAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGT	Oy 1081
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	1861	Q D L	840	AAGAGCTGGCTGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACA	7
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	1741	O D	720 720	1 AGAAGATGCAGCTGGAACAGATGCTCACAGCCCTGGACCAGATGCCGGAGAAGCATTG	Qy 66 Db 66
actact	1681	Db 47	660 660	1 CCCTCAAGAGCCAAGGAGACATGCAGGATCTGAATGGAAACAACCAGTCTGTGACCAGAC	Qy 60 Db 60
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ttggad	1561	D 4	540	1 CAGAGAAGCAGCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATC	Qy 48 Db 48
	1501	Db s	480	1 CGGCAGCCACGGCAGCCAGCAAGGGGGCCAGCCAACCACC	Qy 42 Db 42
	1441	O D CY	420 420	1 CAATGGAAATTGCCCGGATCGTGGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCTCCAGA	Оу 36 Db 36
	1381	Db x	360 360	1 TCTATCAGCACAACCTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGC	Оу 30 Дь 30
gtggg	1321	Db 4	300	ATAATCTCTTGGGTGAAATTGACCAGCAATATAGCCGATTCCTGCAAGAGTCCAATGTCC	Oy 241 Db 241
	1261	Db	240	1 TTGAGAGTCAAGACTGGGGCATATGCAGCCAGCAAGAGAGTCACATGCCACGTTGGTGTTTC	Oy 18

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                  New antisense compound for inhibiting the expression of sitransducer and activator of transcription 3 (STAT3) in celand treating diseases or condition associated with STAT3,
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Query Match Best Local

Local

Similarity

99.8%;

Score Pred.

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Length

2869;

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CC The present invention describes an antisense compound (1), 8 to 30 CC nucleobases in length, that is targeted to a nucleic acid molecule cell encoding STAT3 (Signal Transducer and Activator of Transcription) and CC which inhibits the expression of it. (1) has antiinflammatory, and inhibiting the expression of STAT3 in cells or tissues, treating CC an animal having a disease or condition characterised by a reduction in CC apoptosis, and inducing apoptosis in a cell. Diseases or conditions that are treated are rheumatoid arthritis, cancer of the breast, CC prostate, brain, head and/or neck, leukaemia, myeloma, melanoma or CC lymphoma. (1) can also be used for diagnostic methods in detecting and CC determining the role of STAT3 in various cell functions, physiological CC processes and conditions and for diagnostic methods in detecting and CC diagnostic heroid of STAT3. (1) can be used alone or with other drugs as CC an immunostimulator. (1) is used in sandwich and colourimetric assays, CC involving enzyme conjugation and radiolabeling and is used in CC diagnostic kits. AAC93150 encodes human STAT3 and AAC93231 encodes mouse CC STAT3 as given in the exemplification of the present invention. AAC93151 colour. Octobe which are used in example from the present invention. AAC93151 antisense oligonucleotides, and AAC93299 represents a mismatch control colour.
Sequence
                                                oligonucleotide which are used in example from
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                                                                                                                                                                                                    TCTATCAGCACAACCTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGC
                                                                                                                                                                                                                                                                                       TTGAGAGTCAAGACTGGGCATATGCAGCCAGCAAAGAGTCACATGCCACGTTGGTGTTTC
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                                                                                                                                                                                                                                                                                                                                                                          CCCTCAAGAGCCAAGGAGACATGCAGGATCTGAATGGAAACAACCAGTCTGTGACCAGAC
                              TAGAACAGAAAATGAAGGTGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAA
                                                                                   CAGAGAAGCAGCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATC
                                                                                                                              TGCACCAGCTGTACAGCGACACGTTCCCCCATGGAGCTGCGGCAGTTCCTGGCACCTTGGA
                    tagaacagaaaatgaaggtggtggagaacctccaggacgactttgatttcaactacaaaa
                                                              cagagaagcagcagatgttggagcagcatcttcaggatgtccggaagcgagtgcaggatc
                                                                                                       caatggaaattgcccggatcgtggcccgatgcctgtgggaagagtctcgcctcctccaga
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                                                                                                                                                                                                                                                                           ttgagantraagactgggcatatgcagccagcaaagagtcacatgccacgttggtgtttc
                                                                                                                                                                                                                                                                                                                      tgcaccuyrtyLacagcgacaegttccccatggagctgcggcagttcctggcaccttgga
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1740	CTACTCAGGGTGTCAGATCACATGGGCTAAATTCTGCAAAGAAAAC 	168	Qγ
1680 1680	1 GAGGGCTGAGCATCGAGCAGCTGACAACGCTGGCTGA 	162	DP 6A
1620 1620	1 TTGGAACCTGGGACCAAGTGGCCGA	156 156	D 04
1560 1560	1 TGTGGTATAACATGCTGACCAATAACCCCAAGAACGTGAACTTCTTCACTAAGCCGCCAA	150	Db Qy
1500	1 CCTTGCCAGTTGTGGTGATCTCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATCC	144	D
4 4	TCCAGACTGAGGTTACCACCAAGGCCTCAAGATTGACCTACAGACCC 	1 13	ag Qy
∞ œ	TGGGAATGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGC/ 	13	DP QA
	AGCCTGTCTGCAGAGTTCAAGCACCTGACCCTTAGGGAGCAGAGAT 	126 126	Db Qy
NN	AAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGG 	NN	DP 6A
20	CAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCCC 	14	ОУ
1140 1140	1 TCATCAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGT	08	Db Qy
a a	GTGCCTTCGTGGTGGAGCGCAGCCCTGCATGCCCATGCACCCGGACCGGCCCTTAG 	02	Db Db
NN	GGCCCATGCTGGAGGAGAGGATCGTGGAGCTGTTCAGAAACTTAATGA 		Ωy
0 0	AAGAAACTGGAGGAGCTGCAGCAGAAAGTGTCCTACAAGGGCGACCCTA 		ОУ
900	TCTGCCTGGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCC	841	Оу
840	AAGAGCTGGCTGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACA	781 781	ф
780 780	GGCTCTTGTCAGCAATGGAGTACGTGCAGAAGACACTGACTG	721 721	Db Oy
720 720	AGAAGATGCAGCAGCTGGAACAGATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTG	661 661	Qy Db
6		601	Dβ

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Qу Db	Qy	Фу	Qy Db	Qy Db	Qy	Qу	Оy	Qу	Qy Db	Qу	Qy Db	Qу	Qy Db		Qy Db	Оy	Оy	В
2761 2761	7	2641 2641	2581 2581	2521 2521		4 4	2341 2341	2281 2281	2221 2221	2161 2161		2041 2041	1981 1981	1921 1921	1861 1861	1801 1801	1741 1741	1681
ACCCCATTCTGGGAACTCCTGGCTCTGCACTTTCAACCTTGCTAATATCCACATAGAAGC 2	4 – H	AAAGGGAACACCTCCTGTCCTGCCCGCCTGCCCTTTTTCAGCAGCTCGGGGGTTGG 2	GGGGCTGAGAGCAGAAGGGAGGC 2 	GAGTGTGGGTGATAAAC 2 	TCGTCTGAAACTCCTAACTTTGTGGTTCCAGATTTTTTTT	GCAGAGACGTGACTTGAGACACCTGCCCCGTGCTCCACCCCTAAGCAGCCGAACCCCATA 2	ACATGGATCTGACCTCGGAGTGTGCTACCTCCCCCATGTGAGGAGCTGAAACCAGAAGCT 2	GAAATAACGGTGAAGGTGCTGAGCCCTCAGCAGGAGGGCAGTTTGAGTCGCTCACGTTTG 2	TTAGATTCATTGATGCAGTTTG 2 	TTCATCTGTGTGACACCAACGACCT 2 	CCAAGGAGGAGGCATTTGGAAAGTACTGTAGGCCCGAGAGCCAGGAGCACCCCGAAGCCG 2	IACCTCTACCCCGACATTC 2	CTGAAATCATGATGGGCTATA 2 	VTCAGTGGCAAGACCCAGATCCAGTCTGTAG 1 	TTCAGCGAGAGCAGCAAAGAAGGAG 1 	CTTTGGAATGAAGGGTACATCATGGGTTTCATCAGCAAGGAGCGGGAGCGGGCCATCC 1 	CTTCTCCTTCTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTGG	tcagggtgtcagatcacatgggctaaattctgcaaagaaaacatggctggc
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P-PSDB;
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interleukin-6;
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Local Similarity 99.4%;
nes 2438; Conservative
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DB; AAR82995.
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                                     GGCTCAGTGGAACCAGCTGCAGCAGCTGGACACGCTACCTGAAGCAGCTGCACCAGCT
                                                                      caggccggccagtcgggctccagccccggagacagtcgagacccctgactgcagcaggat
                                                                                        CAGGCCGGCCAGTCGGGCTC--AGCCCGGAGACAGTCGAGACCCCTGACTGCAGCAGGAT
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6; signal transmission; liver; antibody; antisen;
tiinflammatory; antitumor; hypotensive; therapy;
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Similarity 90. 05; Conservative

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         transcription factor related to signal transmission of interleukin-6 (IL-6). Human placenta cDNA is isolated using an IL-6-treated mouse liver polymerase chain reaction product as a cDNA probe. APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary hypertension, etc.
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interleukin-6; signal transmission; placenta; antibody; anti
ribozyme; antiinflammatory; antitumour; hypotensive therapy;
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	coggcgtccagttcactactaaagtcaggttgctggtcaagttccctgagt	23	DЪ
4	CATCAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAG	80	Qy
23	agtgccttgtggtggagcggcagccctgcatgcccatgcatcc	17	Db ?
08	GAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCCGGACC	0	VQ
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1112	tcaacaaattaagaaactggaggagttgcaccaaaagtttcctacaaag	ū	рb
960	CCAACAAATTAAGAAACTGGAGGAGCTGCAGCAGAAAG	901	Qy
1052	ggataacgtcattag	9	DЬ
900	CTGCCTGGACCGTCTGGAAAACTGGATAACTTCATTAG	4	Qy
992	aggagctggctggactggaagaggcggcaacagattgcctgcattggaggcccgccc	933	Db
840	AGAGCTGGCTGACTGGAAGAGGCGGCCAGAGATCGCGT	œ	ОУ
932	agtgagctggcggggctttgtcagcgatggagtacg	7	Db
780	GAGTGAGCTGGCGGGGCTCTTGTCAGCAATGGAGTACG	2	Qy
872	aagatgcagcagctggaacagatgctcactgcgctgg	813	Db
720	GAAGATGCAGCAGCTGGAACAGATGCTCACAGCCCTGG	9	Qy
812	tgcaagatctgaatggaa	753	Db
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752	gaacagaaaatgaaagtggtagagaatctccaggatg	693	Db
600	AGAACAGAAAATGAAGGTGGTGGAGAACCTCCAGGACG.	4	Qy
692	gagaagcagcagatgctggagcagcaccttcaggatg	633	Db
540	AGAGAAGCAGCAGCAGCTTGGAGCAGCATCTTCAGGATG	481	Qy
632	caacc	573	Db
480	GGCAGCCACGGCAGCCAGCAAGGGGGCCAGGCCAACC	421	Qy
572	aatggagattgcccggattgtggcccggtgcctgtggg	513	Db
420	AATGGAAATTGCCCGGATCGTGGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCTCCAG	361	Qy
512	atcagcacaatctacgaagaatcaagcagtttcttcagagcaggtatcttgaga	453	DЬ
360	CTATCAGCACAACCTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTC	301	Qy
452	cagcagtatagccgcttcctgcaagagtcgaatgttc	393	Db
300	TAATCTCTTGGGTGAAATTGACCAGCAATATAGCCGATTCCTGCAAGAGTCCAATGTC	241	Qy
392	tigagagtcaagattgggcatatgcggccagcaagaatcacatgccactttggtgtttc	333	B 2
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180	GCACCAGCTGTACAGCGACACGTTCCCCCATGGAGCTGCGGCAGTTCCTGGCACCTTGGA	121	Qγ

2340	AAATAACGGTGAAGGTGCTGAGCCCTCAGCAGGAGGGCAGTTTGAGTCGCTCACGTTTG	2281	Qy
2432	cattgacctgccgatgtccccccgcgctttagattcattgatgcagtttg		Db
2280	CAGCAATACCATTGACCTGCCGATGTCCCCCCGCACTTTAGATTCATTGATGCAGTTTG	Ν	Qy
2372	gctgcccatacctgaagaccaagtttatctgtgtgacaccaacgacct	2313	Db
2220	CCCAGGTAGTGCTGCCCCGTACCTGAAGACCAAGTTCATCTGTGTGACACCAACGACCT		Qy
31		25	Db .
Ξ.	AGGAGGAGGCATTTGGAAAGTACTGTAGGCCCGAGAGCCAGGAGCACCCCGAAGCCG		Qy
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2100	GATCATGGATGCGACCAACATCCTGGTGTCTCCACTTGTCTACCTCTACCCCGACATT	2041	Q _V
2192	acccatacacaaagcagcagctgaacaacatgtcatttgctgaaatcatcatgggctata	2133	Db
2040	GCCATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGGCTATA	9	Qy
13		07	Db
1980	GGTCACTTTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTAG		Qy
2072	tgagcactaagcccccaggcaccttcctgctgcgcttcagtgaaagcagcagcaaagaaggag	2013	Db
1920	AAGCACAAAGCCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAAGAAGGA	86	Qy
2012	ccctttggaatgaagggtacatcatgggtttcatcagcaaggagcgggagcgggccatct	1953	Db
	CTTTGGAATGAAGGGTACATCATGGGTTTCATCAGCAAGGAGCGGGAGCGGGCCATC	8	Оу
1952	gcttctcctactgggtctggctagacaatatcatcgaccttgtgaaaaagtatatcttgg	œ	Db
1800	TCTCCTTCTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTG	74	Оу
1892	actactcagggtgtcagatcacatgggctaacttctgcaaagaaaacatggctggc	83	Db
1740	CTACTCAGGGTGTCAGATCACATGGGCTAAATTCTGCAAAGAAAACATGGCTGGC	89	Qy
1832	gggggctgagcatcgagcagctgacaacgctggctgagaagctcctagggcctggtgtga	1773	Db
00	AGGGCTGAGCATCGAGCAGCTGACAACGCTGGCTGAGAAAGCTCCTAGGGCCTGGTGTG	6	Ωу
1772	ttggaacctyggaccaagtggccgaggtgctcagctggcagttctcgtccaccaacca	1713	Db
	TGGAACCTGGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCACCACCAAGC	56	Qy
1712	tgtggtacaacatgctgaccaacaatcccaagaatgtgaacttcttcactaagccgccaa		Db
	GTGGTATAACATGCTGACCAATAACCCCAAGAACGTGAACTTCTTCACTAAGCCGCC	50	Оу
1652	ccttglcagttglggtgatctccaacatctgtcagatgccaaatgcctgggcgtccatcc	G	Дb
1500	CTTGCCAGTTGTGGTGATCTCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATC	44	Qy
1592	gattgacctagagacc	1533	Db
1440	GATCACCTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACT	38	Qy
1532	cgagccaattgtgatgcttccctgattgtgactgaggagctgcac	4	Db
1380	TGGGAATGGACGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCACC	1321	Qy
1472	cacttgaccctgagggagcagag	4	Db
1320	GTCTAACAACGGCAGCCTGTCTGCAGAGTTCAAGCCACCTGACCCTTAGGGAGCAGA	N	Qy
1412	ggaaatttaacattctgggcacaaacacaaaagtgatgaacatgg	1353	Db
1260-	CAGAGGGTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAG	1201	Qy

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                                                                                                                                                                                                                                                                                                                                                                                                                     respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhintis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
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oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universat' or alternative base (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities
                                                                                                             Low adenosine (A) content antisense oligonucleotides which trigger adenosine receptors during metabolism, useful e.g. cancers and respiratory obstructions -
                                                                                                                                                                                                                          (UYEC-)
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                                                                                                                                                                     WPI; 2000-679539/66.
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                                                                                   Disclosure;
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CC expression and or activity of target polypeptides associated with CC lung/respiratory disorders and malignancies, such as stimulating and CC activating peptide factors and transmitters, transcription factors. CC immunoglobulins and antibodies, antibody receptors, cytokines and CC chemokines, endogenously produced specific and non-specific enzymes. CC binding proteins, adhesion molecules and their receptors, cytokine and CC chemokine receptors, adenosine receptors, bradykinin receptors, central CC nervous system (CNS) and peripheral nervous and non-nervous system peptide cransmitters, defensins, growth factors, vasoactive peptides and CC receptors, binding proteins and malignancy associated proteins. The CC antisense oligonucleotides may be used in this way to treat disorders cincluding respiratory obstruction (especially pulmonary obstruction cand/or bronchoconstriction) and/or lung inflammation, allergy(les) and/or surfactant hypoproduction which are associated with a disease or CC and/or selected from pulmonary vasoconstriction, inflammation, cc allergies, asthma, impeded respiratory obstructive pulmonary distress syndrome (CC pulmonary transplantation rejection, pulmonary distress syndrome CC pulmonary transplantation rejection, pulmonary distress syndrome CC fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 2787 BP; 729 Α; 719 C; 753 G; 586 .. 0 other;

Query Match Best Local :

Local Similarity

74.7%; 90.9%;

Score 2144.2; Pred. No. 0; Mismatches

DB

21;

Length

0;

223; Indels

7; Gaps

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150 standard;

Human nucleotide sequence SEQ IJ NO:1.

RESULT
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XX AAC9
XX LIS-F
DT 15-F
DT Huma
XX Huma
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XX Huma
XX Huma Human; mouse; STAT3; phosphorothioate; antisense oligonucleot modulation; signal transducer and activator of transcription; DNA-binding protein; signal transduction; inhibition; apoptos inflammatory disease; cancer; antiinflammatory; antirheumatic oligonucleotide;

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CC The present invention describes an antisense compound (I), 8 to 30 cc nucleobases in length, that is targeted to a nucleic acid molecule cc encoding STAT3 (Signal Transducer and Activator of Transcription) and cc which inhibits the expression of it. (I) has antiinflammatory, compound the expression of STAT3 in cells or tissues, treating cc antirheumatic, cytostatic and immunostimulatory activities. (I) is used cf or inhibiting the expression of STAT3 in cells or tissues, treating cc an animal having a disease or condition associated with STAT3 or a cc an animal having a disease or condition associated with STAT3 or a cc an animal having a disease or condition associated with STAT3 or a cc apoptosis, and inducing apoptosis in a cell. Diseases or conditions that are treated are rheumatoid arthritis, cancer of the breast, cc prostate, brain, head and/or neck, leukaemia, myeloma, melanoma or cl lymphoma. (I) can also be used for diagnostic methods in detecting and determining the role of STAT3 in various cell functions, physiological composition of STAT3. (I) can be used alone or with other drugs as cc an immunostimulator. (I) is used in sandwich and colourimetric assays, cc involving enzyme conjugation and radiolabeling and is used in diagnostic kits. AAC93130 encodes human STAT3 and AAC93231 encodes mouse coligonucleotides, and AAC93299 represent STAT3 phosphorothioate antisense oligonucleotides, and AAC93290 represents a mismatch control control article which are used in avance of the present invention. AAC93151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound for inhibiting the expression of signal transducer and activator of transcription 3 (STAT3) in cells or tissues and treating diseases or condition associated with STAT3, such as rheumatoid arthritis and cancer.
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Query Match Best Local

Similarity

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                                            transducer and activator of transcription 3 (STAT-3, see AAB19964).

The invention provides a crystal of a core portion of a STAT protein in dimer form with an 18-mer duplex DNA (see AAAB233) that contains a binding site for the STAT dimer. The core portion of a STAT contains a hinding site for the STAT dimer. The core portion of a state of the state of 
                                                                                                                                                                                                                                                                                                                                                                                                                        Novel crystal useful in drug screening assays, signal transducer, activator of transcription (
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1021 AGAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCACCCGGACCGGCCCTTAG	841 TC 993 tc 901 GC 1053 gt		541 693 601 753		- w - w -	Matches 2305; Conservative 0; Mismatches 223; Indels 7; Gaps 2; 61 GCAGCAGGATGGCTCAGTGGAACCAGCTGCAGCAGCTGGACACACGCTACCTGAAGCAGC 120
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2193 agatcatggatgctaccaatatcctgttgtctccaacttgtctatctctatctctatctctgaattc 2101 ccaaggaggaggcagriiggaaagararggaggcccgaagagccaggagcacccgaagccg	1921 GGGICACTITICACTITGGTTGGAAAAGGACATCAGTGCAAAACCAAAACCAAATCAAATCAATC	d-н 0-0 ч-	1621 GAGGGCTGAGCATCGACACCTGACAACGCTGACAACACTTCCTAGGCCTGACAACACTTCCTAGGCCTGACAACACTTCCTAGGCCTGACAACACTTCCTAGGCCTGACAACACTTCCTAGGCCTAGACACTTCTAGATACTAGATACAACACAAGAAAACATGACAAGAAAACATGACAAGAAAACATGACAAGAAAACATGACAAGAAAACATGACAAGAAAACATGACAAGAAAACATGACAAGAAAACATGACAAGAAAACATGACAAGAAGAAAACATGACAAGAAGAAAACATGACAAGAAGAAAAACATGACAAGAAGAAAACATGACAAGAAGAAAACATGACTGAAAAAACATATATCTTGGAAAAAACATATATCTTGGAAAAAACATATATCTTGGAAAAAACATATATCTTGGAAAAAACATATATCTTGGAAAAAACATATATCTTGGAAAAAACTATATCTTGGAAAAACTATATCTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATCTTTGGAAAAACTATATATCTTTGGAAAAACTATATATCTTTGGAAAAACTATATCTTTTGAAAAACTATATATCTTTTGAAAAACTATATATCTTTTGGAAAAACTATATATCTTTTGAAAAACTATATATCTTTTGAAAAACTATATATCTTTTGAAAAACTATATATCTTTTGAAAAAACTATATATA	т-н т-н о-	1473 gtgggaatgggggccgagccaattgtgatgcttccctgattgtgactgaggagctgcacc 1381 TGATCACCTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACT 1381 TGATCACCTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACT 1381 TGATCACCTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACT 11111111111111111111111111111111	5 5 4 3 4 B

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 2493
Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58104 encode human lung cancer associated proteins and polynucleotide sequences, their agonists, an antagonists may have neuroprotective; cytostatic; cardioactive;
                                                                            Lung cance
                                                                                                                                                        (HUMA-)
                                                                                                                                                                                                                                                                                   cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; prolliferative disorder; wound healing; infectious disease; ds
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                                                Claim
                                                                                                         P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer associated gene sequences, referred gens, useful for treatment, prevention, and
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                                                                                                         2000-587514/55
DB; AAB58442.
                                                                                                                                                                                                                                                                                                                                             cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACTGTTATGTAAA
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ROSEN
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                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                        cancer associated protein;
                                                                                                                                                                                                                                                                                                                                            associated polynucleotide sequence
                                                                                                                                                                                                        2000WO-US05918
                                                                                                                                                        GENOME SCI INC C A.
                                                794-795;
                                                                                                                                                                                      99US-0124270
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muscular active; vulnerary;
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immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous oth diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive,
                                                                         gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences ART18425 - ART18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                       sequences
                                                                                                                                                                                                                                                                                     other
                                                                                                                                                                         and
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Sequence 3156 HР; 832 ۶. 792 c; 826 <u>ი</u> 705 Ţ'; --other;

Query Mai Best Loci Matches

2464;

Conservative

0

Mismatches

334; Indels

51;

Gaps

8

Y Match

Similarity

74.3%; 86.5%;

Score 2132.6; Pred. No. 0;

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21;

Length

밁 õ 밁 Š В Q В γQ B Š 밁 Qy 밁 Ωy B Š 멍 Q В Qy 망 Ş 망 Q DЬ Qy 674 548 614 488 554 428 494 434 308 374 248 314 254 914 788 854 728 794 899 734 368 188 194 89 CTTGC. AATTGCCCGGATCGTGGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCTCCAGACGGCAGC GCACAACCTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGCCAATGGA cctquesemattgaccagcagtatagccgcttcctgcaagaqtcgaatgttctctatca gctctacagtgacagcttcccaatggagctgcggcagtttctggccccttggattgagag GCTGTACAGCGACACGTTCCCCCATGGAGCTGCGGCAGTTCCTGGCACCTTGGATTGAGAG GATGGCTCAGTGGAACCAGCTGCAGCAGCTGGACACACGCTACCTGAAGCAGCTGCACCA 127 gcagcagatgctggagcagcaccttcaggatgtccggaagagagtgcaggatctagaaca GCAGCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATCTAGAACA gattgcccggattgtggcccggtgcctgtgggaagaatcacgccttctacagactgcagc gcacaatctacgaagaatcaagcagtttcttcagagcaggtatcttgagaagccaatgga GGCTGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACATCTGCCT gctggcggggcttttgtcagcgatggagtacgtgcagaaaactctcacggacgaggagct 187 847 913 607 613 487 427 493 367 433 373 247 313 253 973 787 853 727 793 667 733 673 547 553 307

1927 2053	68 AAAGCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAAGAAGGAGGGGTCAC 	Oy 18 Db 19
1867 1993	08 GAATGAAGGGTACATCATGGGTTTCATCAGCAAGGAGCGGGAGCGGGCCATCCTAAGCAC 	Oy 18 Db 19
1807 1933	.748 CTTCTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTGGCCCTTTG	Qy 1:
1747 1873	8 AGGGTGTCAGATCACATGGGCTAAATTCTGCAAAGA 	_
1687 1813	9 – S	
1627 1753	68 CTGGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCACCACCAAGCGA(
1567 1693	B TAACATGCTGACCAATAACCCCAAGAACGTGAACTTCTTG 	Qy 1 Db 1
1507 1633	48 AGTTGTGGTGATCTCC	Qy 1 Db 1
1447 1573	88 CTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAG 	نبو نبو
1387 1513	28 TGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCG 	Qy 1 Db 1
1327 1453	268 CAACGGCAGCCTGTCTGCAGAGTTCAAGCACCTGACCCTTAGGGAGCAGAGAGTGTGGGAA	Oy 1 Db 1
1267 1393	08 GTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGGAGTCT 	1 1
1207 1333	48 TCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCCTCAGA 	Qy 1 Db 1
1147 1273	88 GACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAI	Оу 1 Db 1
1087 1213	gca 	Qy 1 Db 1
1027 1153	968 GCACCGGCCCATGCTGGAGGAGAGGAGTCGTGGAGCTGTTCAGAAACTTAATGAAGAGTGC 	2y .
967 1093	08 AATTAAGAAACTGGAGGAGCTGCAGCAGAA 	Qy Db 1
907 1033	48 GGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCCGCCAACA 	Qy Db

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	TCCTCTTTAAATTAAAAAAAAAAAAAAAAAAAAAAAAA	2840	Ş
 agg 3010		2951	Db
AGG 2839	TCTGCACTTTC-AACCTTGCTAATATCCACATAGAAGCTAGGACTAAGCCCAGG	2783	Qy
tgg 2950	atcettetgeetgtttetgtaageaaatgeeaeaggeeaectatagetaeataeteet	2891	Db
- G	CTGTTGCCCCACTCTGTGAGCTGATACCCCCATTCTGGGAACTCC	2733	Оу
cggc 2890	.ttgttattgttgttgttcttagacaagtgcctcctggtgcctc	2831	Db
rggc 2732	GTTGGTTGTTAGACAAGTGCCTCCTGGTGCCCA	2683	Qy
0	tggctagagggagaaaaggaaatgtcttgtgtttttgtttcccctgccctcct	2771	Db
PTTT 2682	CAAAGGGGAACACCTCTGTCCTGCCGCCT	2636	Qy
11 19999 2770		2711	Дb
N	TATGTAAAGAGGAGAGACCTCTGAGTCTGGGGATGGGGCTGAGAGCAGA		Qy
ettt 2710	tttgagcaatctgggcacttttaaaaatagagaaatgagtgaatgtgggtgatctgc	2651	Db
TGT 2583	TTTGGGCAATCTGGGCACTTTTTAAAAGAGAGAAATGAGTGAG	2524	Qy
Ν	totgaaactactacttgtggttccagatttttttaatctcctacttctgctatc	2594	Db
TATC 2523	TCTGAAACTCCTAACTTTGTGGTTCCAGATTTTTTTTTT	2464	Qy
2	gatacgactgaggcgctacctgcattctgccaccctcacacagccaaaccccaga	2534	Db
ATCG 2463	AGACGTGACTTGAGACACCTGCCCCGTGCTCCACCCCTAAGCAGCCGAACCCCAT	2404	Оу
 aaa 2533	tcccccatgtgaggagctgagaacggaaqctgc	2474	DЪ
24	TCTGACCTCGGAGTGTGCTACCTCCCCCATGTGAGGAGCTGAAACCAGAAGCTGC	2348	Oy
1111 199a 2473	tggtgaaggtgctgaaccctcagcaygagggcagtttgagtccctcacctttgacatgga	2414	Db
TGGA 2347	CGGTGAAGGTGCTGAGCCCTCAGCAGGAGGGCAGTTTGAGTCGCTCACGTTTGACAT	2288	Qy
ataa 2413	taccattgacctgccgatgtccccccgcactttagattcattgatgcagtttggaaataa	2354	Db
ATAA 2287	TACCATTGACCTGCCGATGTCCCCCCCCCCACTTTAGATTCATTGATGCAGTTTGGAAA	2228	Qy
agcaa 2353	ttatctgtgtgacaccaacgacctgca	2294	Db
3CAA 2227	AGTGCTGCCCCGTACCTGAAGACCAAGTTCATCTGTGTGTG	2168	Оу
cagg 2293	ggaggcattcggaaagtattgtcggccagayagccaggagcatcctgaagctgacccagg	2234	DЪ
CAGG 2167	GGAGGCATTTGGAAAGTACTGTAGGCCCGAGAGCCAGGAGCCACCCCGAAGCCGACCC	2108	Qy
ayga 2233	ggatgctaccaatatcctggtgtctccactggtctatctctatcctgacattcccaa	2174	DЬ
AGGA 2107	GGATGCGACCAACATCCTGGTGTCTCCACCTTGTCTACCTCTACCCCGGACATTCCCCAAGG	2048	Qy
tcat 2173	cacaaagcagctgaacaacatgtcatttgctgaaatcatcatgggctataagat	2114	DЬ
TCAT 2047	CAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGGCTATAAG <i>I</i>	1988	Qy
cata 2113	tttcacttgggtggagaaggacatcagcggtaagacccagatccagtccgtggaaccata	2054	Db
CATA 1987	TTTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTAGAGCC	1928	Qγ

RESULT 10 AAA34938 ID AAA34938 standard; DNA; 2847 BP. XX

AAA34938

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cc fibrosis, pulmonary hypertension, emphysema, chronic obstructive
cc pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
cc carcinomas, and cancers which may metastasise to the lungs, including
cc breast and prostate cancer. The reduction of the adenosine content of
ct the ONs reduces side effects. The A-containing ONs break down with the
cr release of deoxyadenosine which activates adenosine receptors causing
cc monchoconstriction and inflammation. AAA32312 to AAA35312 represent the
cc invention, which correspond to SEQ ID NO:1 to 2815, and then the last
cc invention, which correspond to SEQ ID NO:1 to 2815, and then the last
cc invention. N.B. Sequences given in the disclosure of the present
cc invention. N.B. Sequences given in the disclosure of the present
cc invention to AAA3392) are specifically claimed ONs from the present
cc invention to B. Sequences given in the disclosure of the present
cc invention do not match up with their corresponding SEQ ID NO: sequences
cc given in the sequence listing.
      Query Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoonstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung diseases and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosic conditions, respiratory distress syndrome, pain, cystic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                             Sequence
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The present sequence represents a cDNA encoding a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. This sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 DNA molecule can be used for the recombinant express of the variant. STAT3 protein is useful as a medicament or pharmaceuti
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109 GAGGCATTTGGAAAGTACTGTAGGCCCGAGAGCCAGGAGCACCCCGAAGCCGACCCAGGT 21	1981 gatgctaccaatatcctggtgtctcccactggtctatctctatcctgacattcccaaggag 20	049 GATGCGACCAACATCCTGGTGTCTCCACTTGTCTACCCTCTACCCCGACATTCCCAAGGAG 21	21 acaaagcagctgaacaacatgtcatttgctgaaatcatgggctataagatcatg 19	вът пластидувгудаванувасалсавсув ганунсскав постолнатала праводата с ту	929 TTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTAGAGCCCATAC 19		869 AAGCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAAGAAGGAGGGGTCACT 19		18	1749 TTCTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTGGCCCCTTTGG 18	16	1689 GGGTGTCAGATCACATGGGCTAAATTCTGCAAAGAAAACATGGCTGGC		16		GGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCACCACCAAGCGAGGGGCTG 16	1509 AACATGCTGACCAATAACCCCAAGAACGTGAACTTCTTCACTAAGCCGCCAATTGGAACC 15	381 gttgtgglgatctccaacatctgtcagatgccaaatgcctgggcgtccatcctgtggtac 14	449 GTTGTGGTGATCTCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATCCTGTGGTAT 15	1321 tttgagaccgaggtgtatcaccaaggcctcaagattgacctagagacccactccttgcca 13	GAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGAGACCCACTCCTTGCCA 14	ggccgagccaattgtgatgcttccctgattgtgactgaggagctgcacctgatcacc 13	13		13	caac 12	12	1081 cagcttaaaattaaagtgtgcattgacaaagactctggggacgttgcagctctcagagga 11	12	1089 ACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGTTGAATTAT 11	10	GTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCGGGACCGGCCCTTAGTCATCAAG 10
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                                                                                                                                A CDNA clone (AAT31278) codes for mouse signal transducer and activator of transcription (STMT) protein STMT1 (AAW03172), a homologue of human STMT1-alpha (AAW03168), that serves a dual purpose, i.e. signal transduction from ligand activated receptor
                                                                                                                                                                                                                                                                                      New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity
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                                                                                     nase complexes followed by nuclear translocation and DNA binding activate transcription. STAT1 includes a DNA-binding domain
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            CAAGGAGGAGGCATTTGGAAAGTACTGT
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caaagaccacgcctttgggaagtattat
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RESULT

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24-SEP-1993;
11-MAR-1994;
11-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A fragment encoding the human Stat91 protein was used to scree murine thymus and spleen cDNA for homologous proteins. A high homologous gene (given in AAQ89338) was isolated that encoded 91 kDa protein (AAR72080) (Stat1) that was responsive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays a for treating cellular debilitations, derangements and/or dysfunctions, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal transducer and activator of transcription; Stat91; receptor recognition factor; transcription cellular dehilitation; derangement; dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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cctcctctcacagctggacgaccagtacagccgcttttctctggagaataatttcttgtt
                                           TCTCTTGGGTGAAATTGACCAGCAATATAGCCGATTCCTGCAAGAGTCCAATGTCCTCTA
                                                                                    aaagcaagactgggagcacgcttctatgatgtctcgtttgcgaccatccgcttccatga
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94US-0212185.
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RESULT 1 AAC98863 ID AAC9 AAC98863 standard; cDNA; 2974 ВР

09-MAR-2001

(first

entry)

pancreatic

cancer antigen nucleotide sequence SEQ

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antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss. detection; diagnosis; identification; cytostatic; neu nootropic; immunomodulatory; relaxant; contraceptive; pancreas; pancreatic cancer; pancreatic cancer antigen; diagnosis; identification; cytostatic; neuroprotective; gynaecological;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hypridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins, called pancreatic cancer antigens, given in AAB54008 AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contrac gynaecological, cardiant and antiinflammatory activities, and c in gene therapy. The polynucleotide and proteins can be used fo preventing, treating, or ameliorating a medical condition or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a nathological condition.
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cttggatcagctgcagaactggttcactatagttgcggagagtctgcagcaagttcggca CCTGGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCCGCCA actagtggagtggaagcggagacagcagagcgcctgtattgggggggccgcccaatgcttg GATGCAGCTGGAACAGATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTGTGAG gcagaacaqagaacac----gagaccaatggtgtggcaaagagtgatcagaaacaaga ACAGAAAATGAAGGTGGTGGAGAAACCTTCCAGGACGACTTTGATTTCAACTACAAAACCCT GAAGCAGCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATCTAGA acagcataacataaggaaaagcaagcgtaatcttcaggataattttcaggaagacccaat CACCTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACTCCTT CAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGTTGAA 1144 aaaaaacaaacaagtgttatgggaccgcaccttcagtcttttccagcagctcattcagag ACAAATTAAGAAACTGGAGGAGCTGCAGCAGAAAGTGTCCTACAAGGGCGACCCTATCGT GCTGGCTGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACATCTG caaaataulagagttgctgaatgtcactgaacttacccagaatgccctgattaatgatga acagctqttactcaagaagatgtatttaatgcttgacaataagagaaaggaagtagttca gcatgaaatcaagagcctggaagatttacaagatgaatatgacttcaaatgcaaaacctt caaacayaaagcttgacagtaaagtcagaaatgtgaaggacaaggttatgtgtätaga ccagagatttaatcaggctcagtcggggaatattcagagcaca-----gtgatgttaga ccagatgtctatgatcatttacagctgtctgaaggaagaaaggaaaattctggaaaacgc GGAAATTGCCCGGATCGTGGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCTCCAGACGGC 424 AGGGTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGGAGTC TTATCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCCTCAG ctcgtttgtggtggaaagacagccctgcatgccaacgcaccctcagaggccgctggtctt TGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCGGACCGGCCCTTAGTCAT GCAGCACCGGCCCATGCTGGAGGAGAGGATGGTGGAGCTGTTCAGAAAACTTAATGAAGAG tagttttgaaacccaattgtgccagcctggtttggtaattgacctcgagacgacctctct GAATGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCACCTGAT caccaatggcagtctggcggctgaatttcggcacctgcaattgaaagaacagaaa.... TAACAACGGCAGCCTGTCTGCAGAGTTCAAGCACCTGACCCTTAGGGAGCAGAGATGTGG aggatttaggaagttcaacattttgggcacgcacacaaaagtgatgaacatggaggagtc ttataat!tgaaagtcaaagtcttatttgataaagatgtgaatqagagaaatacagtaaa gaagacagyggtccagttcactgtgaagttgagactgttggtgaaattgcaagagctgaa gcagctilaaaagttggaggaattggaacagaaatacacctacgaacatgaccctatcac 1175 -aatgctggcaccagaacgaatgagggtcctctcatcgttactgaagagcttcactccct 484 1204 1055 1444 1530 1475 1415 1355 1084 1235 1024 1115 995 784 935 724 664 821 604 761 544 701

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KW Star
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24-SEP-1993;
11-MAR-1994;
11-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences of cDNA encoding receptor regonition factors having mol.wt. of 113 kDa (Stat113), 91 kDa (Stat92) and 84 kDa (Stat84) are given in AAQB935-37 and the deduced amino acid sequences of to STAT proteins in AAR72077-99. These ISGF-3-derived proteins are activated by binding of interferon-alpha (all 3 Stat proteins) or interferon-gamma (Stat91) to cell receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays a for treating cellular debilitations, derangements and/or dysfunctions, etc.
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P-PSDB; AAR72079.
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cttgacagtaaagtcagaaatgtgaaggacaaggttatgtgtatagagcatgaaatcaag
                TTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATCTAGAACAGAAAATGAAG
                                                                             CAGCAAGGGGCCCAGCCCAACCACCCCCGCCGTAGTGACAGAGAAGCAGCAGATG
                                                                                                     atcatttacagctgtctgaaggaagaaaggaaaattctggaaaacgcccagagatttaat
                                                                                                                                                        aggaaaagcaagcgtaatcttcaggataattttcaggaagacccaatccagatgtctatg
                                                                                                                                                                                                                                                             gagcacgctgccaatgatgtttcatttgccaccatccgttttcatgacctcctgtcacag
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                                                   ggctcagtcggggaatattcagagcacagtgatgttagacaaacagaaagag
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94US-0212185.
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Pred. No. 3.2e-177;
0; Mismatches 839;
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1697	CAGCTGACAACGCTGGCTGAGAAGCTCCTAGGGCCTGGTGTGAACTACTCAGGGTGTCAG	1638
1637 1747	GTGGCCGAGGTGCTCAGCTGCCAGTTCTCGTCCACCACCAAGCGAGGGCTGAGCATCGAG	
1577 1687	ACCAATAACCCCAAGAACGTGAACTTCTTCACTAAGCCGCCAATTGGAACCTGGGACCAA	6 5
1517 1627	ATCTCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATCCTGTGGTATAACATGCTG	
1457 1567	GAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACTCCTTGCCAGTTGTGGTG	υrw
1397 1507	GTGACTGAGGAGCTGCACCTC gttactgaagagcttcactcc	1338 1448
1337 1447	CTGACCCTTAGGGAGCAGAGATGI 	1278 1394
1277 1393	ACATGGAGGAGTCTAACAACGGCAG 	1218 1334
1217 1333	GGAT tgag	1158 1274
1157 1273	CAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGTTGAATTATCAGCTTAAA	1098 1214
1097 1213	GAGCGGCAGCCCTGCATGCCCATGCACCGGGACCGGCCCTTAGTCATCAAGACTGGTGTC	1038 1154
1037 1153	ATGCTGGAGGAGAGGATCGTGGAGCTGTTCAGAAACTTAATGAAGAGTGCCTTCGTGGTG	978 1094
977 1093	GTGTCCTACAAGGGCGACCCTATCGTGC tacacctacgaacatgaccctatcacaa	918 1034
917 1033	GAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCCGCCAACAAATTAAGAAA	858 974
857 973	AAGAGGCGGCCAGAGATCGGCGTGCATCGGAGGCCCTCCCAACATCTGCCTGGACCGTCTG	798 914
797 913	ATGGAGTACGTGCAGAAGACACTGACTGATGAAGAGCTGG 	738 854
737 853	CAGATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTGTGAGTGA	678 794
677 793	ATGCAGGATCTGAATGGAAACAACCAGTCTGTGACCAGACAC 	618 740
617 739	TGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAACC	558

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> QΥ δÃ Qy Ъ ρ В Ş В Qy 밁 δÃ 밁 В Š В Ъ 1758 1805 1938 1985 1878 1925 1818 1865 1748 2115 TTTGGAAAGTACT 2127 ||||||||| 2225 tttggaaagtatt 2237 1995 CAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGGCTATAAGATCATGGATGCG 2054 1698 2045 GGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAGAGAGGAGGGGGTCACTTTCACTTGG 1937 TACATCATGGGTTTCATCAGCAAGGAGCGGGAGCGGGCCATCCTAAGCACAAAGCCCCCG 1877 attccgtggacgaggttttgtaaggaaaatataaatgataaaaattttcccttctggctt 1864 ATCACATGGGCTAAATTCTGCAAAGAAAACATGGCTGGCAAGGGCTTCTCTCTGGGTC ACCAACATCCTGGTGTCTCCACTTGTCTACCCCGACATTCCCAAGGAGGAGGA 2114 GTGGAAAAGGAC---ATCAGTGGCAAGACCCAGATCCAGTCTGTAGAGCCATACACCAAG TGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTGGCCCTTTGGAATGAAGGG 1817 cagclgaacatgttgggagagaagcttcttggtcctaacgccagccccgatg---gtctc gagaatattcctgagaatcccctgaagtatctgtatccaaatattgacaaagaccatgcc 2224 aaagaactttctgctgttactttccctgacatcattcgcaattacaaagtcatggctgct gtggagcggtcccagaacggaggcgaacctgacttccatgcggttgaaccctacacgaag tgcatcatgggcttcatcagcaaggagcgagagcgtgccctgttgaaggaccagcagccg tggattgaaagcatcctagaactcattaaaaaacacctgctccctctctggaatgatggg 1924 1994 1804 1984 2164 2104

Search completed: March 19, 2002, 15:21:55 Job time: 4857 sec

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  Sequence
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TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: MOUSE
TYPE: ORGANISM: MOUSE

IMMEDIATE SOURCE: LIBRARY: CLONE: N

Murine 19sf6 splenic/thymic

RESULT US-08-369-796-11 US-08-369-796-11 US-08-369-796-11 Sequence 11, Application US/08369796 Patent No. 5716622 GENERAL INFORMATION: APPLICANT: Zilong Wen APPLICANT: Zilong Wen APPLICANT: Zilong Wen APPLICANT: Zilong Zhong ITILE OF INVENTION: TRANSDUCER AND ACTIVE REGIONS OF TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRI UMBBER OF SEXUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSEE: Klauber 6 Jackson STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTY: USA ZIP: 07601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/369,796 FILLING DATE: 06-JAN-1995 CLASSIFICATION NUMBER: US/08/369,796 FILLING DATE: 06-JAN-1995 CLASSIFICATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-116 TELECOMMUNICATION INFORMATION: TELEFANX: 201 343-1684 TELEX: 133521 INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 2869 base pairs	28 672.6 23.4 2607 3 US-08-956-652-5 29 672.6 23.4 2607 3 US-08-956-869-5 30 672.6 23.4 2607 3 US-08-948-47-5 31 672.6 23.4 2607 5 PCT-US95-17025-5 32 672.6 23.4 3943 1 US-08-369-796-3 34 672.6 23.4 3943 2 US-08-852-091-3 35 672.6 23.4 3943 3 US-08-956-652-3 36 672.6 23.4 3943 3 US-08-956-652-3 37 672.6 23.4 3943 3 US-08-956-652-3 38 672.6 23.4 3943 3 US-08-956-652-3 39 672.6 23.4 3943 3 US-08-956-652-3 39 672.6 23.4 3943 4 US-09-087-465-1 40 666.2 23.2 3943 4 US-09-087-465-1 564.4 19.7 2375 1 US-08-369-796-9 42 564.4 19.7 2375 2 US-08-852-0794-9 43 564.4 19.7 2375 3 US-08-956-652-9 45 564.4 19.7 2375 3 US-08-956-652-9 45 564.4 19.7 2375 3 US-08-956-652-9
TRANSCRIPTION (STAT) PROTEINS	Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 9, Appli

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                                                                                                    Sequence 11, Applicat
Patent No. 5883228
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zibong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Chong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT)
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber 6 Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
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                                                                                                                                                                                                                                                                                AGATCATGGATGCGACCAACATCCTGGTGTCTCCACTTGTCTACCCTCTACCCCCGACATTC
                                                                                                                                                                             TGTTATGTAAAGAGGAGACCTCTGAGTCTGGGGGATGGGGCTGAGAGAGCAGAAGGGAGC
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; NAME/KEY:
; LOCATION:
US-08-852-091-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 2869; Conserv
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COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2869 Dasc r-
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Monse
IMMEDIATE SOURCE:
LIBRARY: splenic/thymic
CLONE: Murine 19sf6
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                 361
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CAATGGAAATTGCCCGGATCGTGGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCCAGA
                                               GCAGCAGGATGGCTCAGTGGAACCAGCTGCAGCAGCTGGACACACGCCTACCTGAAGCAGC 120
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1500 1500	CCTTGCCAGTTGTGGTGATCTCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATCC	1441 1441	Дb
1440 1440	TGATCACCTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGAGACCCACT	w w	Db Qy
1380 1380	GTGGGAATGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCACC	1321 1321	Qy Db
1320 1320	AGTCTAACAACGGCAGCCTGTCTGCAGAGTTCAAGCACCTGACCCTTAGGGAGCAGAGAT	1261 1261	Qy Db
1260 1260	TCAGAGGGTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGG	1201 1201	Qу
1200 1200	TGAATTATCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCC	1141 1141	Qy Db
1140 1140	TCATCAAJACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTT7CCTGAGT	1081	Qу
1080	AGAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCCGGACCGGCCCTTAG	1021 1021	Оy
1020 1020	TCGTGCAGCACCGGCCCATGCTGGAGGAGAGCATCGTGGAGCTGTTCAGAAACTTAATGA	961 961	Оy
960	GCCAACAATTAAGAAACTGGAGGAGCTGCAGCAGAAAGTGTCCTACAAGGGCGACCCTA	901	Оу
900	TCTGCCTGGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCC	841 841	Оу
840	AAGAGCTGGCTGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACA	781 781	Оу
780 780	TGAGTGAGCTGGCGGGGCTCTTGTCAGCAATGGAGTACGTGCAGAAGACACTGACTG	721 721	Оу
720 720	AGAAGATGCAGCAGCTGGAACAGATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTG	661 661	Оу
660	CCCTCAAGAGCCAAGGAGACATGCAGGATCTGAATGGAAACAACCAGTCTGTGACCAGAC (601	Оу
600	TAGAACAGAAAATGAAGGTGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAA (541 541	Оy
540	CAGAGAAGCAGCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATC :	481 481	Qy
480	CGGCAGCCACGGCAGCCAGCAAGGGGGCCAGGCCAACCACC	421 421	Оу
420	CAATGGAAATTGCCCGGATCGTGGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCTCCAGA 4	361	DЬ

2580 2580	ATCTTTGGGCAATCTGGGCACTTTTTAAAAGAGAGAAATGAGTGAG	2521 2521	Qy Db
2520 2520	TGGTCTGAAACTCCTAACTTTGTGGTTCCAGATTTTTTTT	4 4	Qy Db
2460 2460	GCAGAGACGTGACTTGAGACACCTGCCCCGTGCTCCACCCCTAAGCAGCCGAACCCCATA	2401 2401	Qy Db
2400	ACATGGATCTGACCTCGGAGTGTGCTACCTCCCCCATGTGAGGAGCTGAAACCAGAAGCT	ليا ليا	Оу
2340 2340	GAAATAACGGTGAAGGTGCTGAGCCCTCAGCAGGAGGGCAGTTTGAGTCGCTCACGTTTG		Qу
2280 2280	GCAGCAATACCATTGACCTGCCGATGTCCCCCCCGCACTTTAGATTCATTGATGCAGTTTG	2221 2221	Оу
2220	ACCCAGGTAGTGCTGCCCCGTACCTGAAGACCAAGTTCATCTGTGTGACACCAACGACCT	2161 2161	Оу
2160 2160	CCAAGGAGGAGCATTTGGAAAGTACTGTAGGCCCGAGAGCCAGGAGCACCCCGAAGCCG	2101	Qу Db
2100 2100	AGATCATGGATGCGACCAACATCCTGGTGTCTCCACTTGTCTACCTCTACCCGACATTC	2041	Оу Db
2040	AGCCATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGGCTATA	86 86	Оу
1980 1980	GGGTCACTTTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTAG	1921 1921	Qy Db
1920 1920	TAAGCACAAAGCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAAGAAGAAGAG	1861 1861	Qу
1860 1860	CCCTTTGGAATGAAGGGTACATCATGGGTTTCATCAGCAAGGAGCGGGAGCGGGCCATCC	1801	Qy Db
1800	GCTTCTCCTTCTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTGG 	1741 1741	Qу
1740 1740	ACTACTCAGGGTGTCAGATCACATGGGCTAAATTCTGCAAAGAAAACATGGCTGGC	1681 1681	Фр
1680 1680	GAGGGCTGAGCATCGAGCAGCTGACAACGCTGGCTGAGAAGCTCCTAGGGCCCTGGTGTGA	1621 1621	оу оь
1620 1620	TTGGAACCTGGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCACCACCACCAGC	1561 1561	Qy Db
1560 1560	TGTGGTATAACATGCTGACCAATAACCCCAAGAACGTGAACTTCTTCACTAAGCCGCCAA 	1501 1501	Qy

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Sequence 11, Application of the control of the cont
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FILING DATE: 19-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Winn'yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGN
TITLE OF INVENTION: SEQUENCES AND MINUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO U:
FILING DATE: 19-MAR-1993
                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Klauber & Jackson
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CITY: Ha
STATE: 1
COUNTRY:
ZIP: 07
                     TELEX:
                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCCCATTCTGGGAACTCCTGGCTCTGCACTTTCAACCTTGCTAATATCCACATAGAAGC
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VENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
VENTION: SEQUENCES AND METHODS OF USE THEREOF
SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        WO US93/02569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
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Matches 2869; Conserv
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LENGTH: 2869 base pair
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IMMEDIATE SOURCE:
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Page 6

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ATCATCGACCTTGTGAAAAAGTATA 	GCTTCTCCTTCTGGGTCTGGCTAGACAATATV	1741 1741	Оу
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AAGAACGTGAACTTCTTCACTAAG 	TGTGGTATAACATGCTGACCAATAACCCC TGTGGTATAACATGCTGACCAATAACCCC	1501 1501	ду Дъ
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GCCTCCTTGATCGTGACTGAGGAGC	GTGGGAATGGAGCCGTGCCAATTGTGAT 		Qγ
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AGGATCGTGGAGCTGTTCAGAAACTT 	TCGTGCAGCACCGGCCCATGCTGGAGGAG	961 961	Qу
CAGCAGAAAGTGTCCTACAAGGGCGA 	GCCAACAAATTAAGAAACTGGAGGAGCTGC 	901 901	Qy Db
ATAACTTCATTAGCAGAATCTCAACTTCA 	TCTGCCTGGACCGTCTGGAAAACTGGATA TCTGCCTGGACCGTCTGGAAAACTGGATA	841 841	Qу
GAGATCGCGTGCATCGGAGGCCCTCC 	AAGAGCTGGCTGACTGGAAGAGGCGGCCAG	781 781	Db Db
ATGGAGTACGTGCAGAAGACACTGA	TGAGTGAGCTGGCGGGGCTCTTGTCAGCAA	721	Db

	TAGGACTAAGCCCAGGAGGTTCCTCTTTAAATTAAAAAAAA	2821 2821	Оу
2820 2820	ACCCCATTCTGGGAACTCCTGGCTCTGCACTTTCAACCTTGCTAATATCCACATAGAAGC 2	2761 2761	Qу
2760 2760	TTGTTAGACAAGTGCCTCCTGGTGCCCATGGCTACCTGTTGCCCCACTCTGTGAGCTGAT 2	2701 2701	Qу
2700 2700	AAAGGGAACACCTCCTGTCCTGCCCGCCTGCCCTTTTTCAGCAGCTCGGGGGTTGG 2	2641 2641	Db dg
2640 2640	TGTTATGTAAAGAGGAGAGACCTCTGAGTCTGGGGATGGGGCTGAGAGCAGAAGGGAGGC 2	2581 2581	Оу
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2520 2520	TCGTCTGAAACTCCTAACTTTGTGGTTCCAGATTTTTTTT		Дb
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RESULT 4 US-08-956-652-11 ; Sequence 11, Application US/08956652

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Matches 2869
                                                                                                  NAME/KEY:
LOCATION:
S-08-956-652-11
                                                                                                                                    ORGANISM: MOUSE
IMMEDIATE SOURCE:
LIBRARY: Splenic/thymic
CLONE: Murine 19sf6
FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
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GENERAL INFORMATION:
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2869 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR 1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US 08/126,588
FILING DATE: 24-SEP-193
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian Yuan
APPLICANT: Wen, Zilong
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                        HYPOTHETICAL: I
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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                                                                                                                                                                                                                                                   MOLECULE TYPE:
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STREET: 41
CITY: Hack
STATE: New
COUNTRY: U
                                                                                                                                                                                                                                                                              TYPE: nucleic STRANDEDNESS:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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       GCCGCGACCAGCCAGGCCGGCCAGTCGGGCTCAGCCCGGAGACAGTCGAGACCCCTGACT 60
                                   cal Similarity
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AAAAAAA 2869	TAGGACTAAGCCCAGGAGGTTCCTCTTTAAATTAAAAAAAA	2821	Qy
CTAATATCCACATAGAAGC 2820	ACCCCATTCTGGGAACTCCTGGCTCTGCACTTTCAACCTTGCTAATATCCACATAGAAGC	2761	Db
CTAATATCCACATAGAAGC 2820	ACCCCATTCTGGGAACTCCTGGCTCTGCACTTTCAACCTTGCTAATATCCACATAGAAGC	2761	Qy
CCCACTCTGTGAGCTGAT 2760	TTGTTAGACAAGTGCCTCCTGGTGCCCATGGCTACCTGTTGCCCCACTCTGTGAGCTGAT	2701	Db
CCCCACTCTGTGAGCTGAT 2760	TTGTTAGACAAGTGCCTCCTGGTGCCCCATGGCTATCCTGTTGCCCCCACTCTTGTGAGCTGAT	2701	γQ
TCAGCAGCTCGGGGGTTGG 2700	AAAGGGGAACACCTCCTGTCCTGCCCGCCTGCCCTTCTTTTCAGCAGCTCGGGGGTTGG	2641	DЪ
TCAGCAGCTCGGGGGTTGG 2700	AAAGGGGAACACCTCCTGTCCTGCCCGGCCTGCCCTTCTTTTCAGCAGCTCGGGGGTTGG	2641	Qy
CTGAGAGCAGAAGGGAGGC 2640	TGTTATGTAAAGAGGAGAGACCTCTGAGTCTGGGGATGGGGCTGAGAAGGAAG	2581	DЪ
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GTGAGTGTGGGTGATAAAC 2580	ATCTTTGGGCAATCTGGGCACTTTTTAAAAAGAGAGAAATGAGTGAG	2521	DЬ
GTGAGTGTGGGTGATAAAC 2580	ATCTTTGGGCAATCTGGGCACTTTTTAAAAGAGAGAAATGAGTGAG	2521	Qy
TTAATTTCCTACTTCTGCT 2520	TCGTCTGAAACTCCTAACTTTGTGGTTCCAGATTTTTTTT	2461	Db
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TAAGCAGCCGAACCCCATA 2460	GCAGAGACGTGACCTTGAGACCCCGTGCCCCGTGCCCCCATAGCCAGCC	2401	Db
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GGAGCTGAAACCAGAAGCT 2400	ACATGGATCTGACCTCGGAGTGTGCTACCTCCCCCATGTGAGGGGGCTGAAACCAGAAGCT	2341	Db
GGAGCTGAAACCAGAAGCT 2400	ACATGGATCTGACCTCGGAGTGTGCCTACCCCCCATGTGAGGAGCTGAAACCAGAAGCT	2341	Qy
TTTGAGTCGCTCACGTTTG 2340	GAAATAACGGTGAAGGTGCTGAGCCCTCAGCAGGAGGGCAGTTTGAGTCGCTCACGTTTG	2281	рb
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GATTCATTGATGCAGTTTG 2280	GCAGCAATACCATTGACCTGCCGATGTCCCCCCCCCCCC	2221	DЬ
GATTCATTGATGCAGTTTG 2280	GCAGCAATACCATTGACCTGCCGATGTCCCCCCCGCACTTTAGATTCATTGATGCAGTTTG	2221	Qγ

RESULT 5
US-08-956-869-11
Sequence 11, Application US/08956869
Patent No. 6030808
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E. APPLICANT: Chindler, Christian W. APPLICANT: Fu, Xian-Yuan APPLICANT: Fu, Xian-Yuan APPLICANT: Fu, Xian-Yuan APPLICANT: Fu, Xian-Yuan APPLICANT: For, Xilong APPLICANT: Darnell RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: 411 Hackensack Avenue
CITY: Hackensack
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/956,869

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CLASSIFICATION:
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2869 base pairs
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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HYPOTHETICAL:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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LIBRARY: splenic/thymic
CLONE: Murine 19sf6
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STRANDEDNESS: both
TOPOLOGY: unknown
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APPLICATION NUMBER: U
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481	481 CAGAGAAGCAGCAGATGTTGGAGCAGCATCTTCAGGATGTCCCGGAAGCGAGTGCAGGATC 540	40
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541	TAGAACAGAAAATGAAGGTGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAA 600	00
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601	CCTCAAGAGACATGCAGGATCTGAATGUAAACAACCAGTCTGTGACCAGAC 660	60
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Patent No. 6
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                           APPLICATION NUMBER: WO US93/G
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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APPLICANT: Zhong, Zhong
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
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STREET: 11
CITY: 11 Ck
STATE: New
COUNTRY: 10
ZIP: 07601
                      TELEPHONE: 201 %.
TELEPHONE: 201 343-1684
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LENGTH: 28
TYPE: Nucl
STRANDENNES
TOPOLOGY:
NOLECULE TYPE
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOUR
ORGANISM:
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CLONE: MUT
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Best Local Similarity 100.0%;
Matches 2869; Conservative 0
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ORGANISM: Mouse
IMMEDIATE SOURCE:
LIBRARY: splenic/thyn
CLONE: Murine 19sf6
FEATURE:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
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Pred. No. 0;
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APPLICANT:
APPLICANT:

Curt M. Horvath Zhong Zhong Zilong

James E. Darnell,

Jr.

Wen

APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:

OF SIGNAL TRANSCRIPTION (STAT) PROTEINS

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PCT-US95-17025-11
; Sequence 11, Application PC/TUS9517025
; GENERAL INFORMATION:

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PCT-US95-17025-11
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 343-1684
TELEPAX: 201 343-1684
TELEPX: 133521
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 2869; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/17025
FILING DATE: 28-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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  LIBRARY: splenic/thymic
  CLONE: Murine 19sf6
  FEATURE:
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LENGTH: 2869 base pairs
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CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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              TTGAGAGTCAAGACTGGGCATATGCAGCCAGCAAAGAGTCACATGCCACGTTGGTGTTTC
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                                                         TGCACCAGCTGTACAGCGACACGTTCCCCATGGAGCTGCGGCAGTTCCTGGCACCTTGGA 180
New Jersey
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Pred. No. 0;
0; Mismatches
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200	1141 TGAATTATCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCC 1	
140	1081 TCATCAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGT 1 	<u>بر</u> بر
080	1021 AGAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCCGGACCGGCCCTTAG 1	
020	961 TCGTGCAGCACCGGCCCATGCTGGAGGAGAGGATCGTGGAGCTGTTCAGAAACTTAATGA 1 	
60	901 GCCAACAATTAAGAAACTGGAGGAGCTGCAGCAGAAAGTGTCCTACAAGGGGGAGCCTA 9 	
00	841 TCTGCCTGGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCC 9 	
40	781 AAGAGCTGGCTGACTGGAAGAGGCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACA 8	
80	721 TGAGTGAGCTGGCGGGGCTCTTGTCAGCAATGGAGTACGTGCAGAAGACACTGACTG	
20	661 AGAAGATGCAGCAGCTGGAACAGATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTG 7	
60	601 CCCTCAAGAGCCAAGGAGACATGCAGGATCTGAATGGAAACAACCAGTCTGTGACCAGAC 6	
00	541 TAGAACAGAAAATGAAGGTGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAA 6 	
40	481 CAGAGAAGCAGCAGATGTTGGAGCAGCATCTTCAGGATGTCCGGAAGCGAGCTGCAGGATC 5	
80	421 CGGCAGCCAGCGAGCCAGCAAGGGGGCCAGGCCAACCACC	
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60	301 TCTATCAGCACAACCTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGC 3 +	
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1321 GTGGGANTGJAGGCCGTGCCANTGTGATTCGTATTCGTATCGTATCGTACTGAGGACTGAGAGCTGCAA 1381 TGATCACCTTTGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTTAGAGACCCAA 1381 TGATCACCTTTGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCAA 1481 CCTTGCCACTTTGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCAA 1481 CCTTGCCACTTTGAGACTGAGGTGACCACACACCTCTGTCATCACCAAATGCTTGAGCCTAAAGCCACATCAATT 1481 CCTTGCCACTTTGAGACTGAGTCTACCACCAACACCTCTGTCACAATGCCTTGACCAAATGCTTGACCTAAAGCCCAATTAACCCACAATTAACCACACATCTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAATTAACCACAAATTAACAATTAAAAAA	21 GCAGCAATACCATTGACCTGCCGAGTGTCCCCCCGCACTTTAGATTCATTGATGCAGTTTT	22	
1321 GTGGGANTGJAGGCCGTGCCAATTGTGATGCTCCTTGATCGTACTGACTG	1 ACCCAGGTAGTGCTGCCCCGTACCTGAAGACCAAGTTCATCTGTGTGACACCAACGACC	21 21	
1321 GTGGGANT-GAGGCCGTGCCAATTGTGATGCTCCTTGATCGTGACTGAGGAGCTGCACTAGATGAGGACCTGCAATTGTGATCGTCACTGACTG	01 CCAAGGAGGAGGCATTTGGAAAGTACTGTAGGCCCGAGAGCCAGGAGCACCCCGAAGCC 	21	
1321 GTGGGAATGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCAATIGITIIIIIIIIII	1 AGATCATGGATGCGACCAACATCCTGGTGTCTCCACTTGTCTACCTCTACCCCCGACATT	20	
1321 GTGGGAATGGGGCGTGCCAATTGTGATGCCTCTTGATCGTGACGAGGAGCTGCACACCACCACCACCACCACCACCACCACCACCACCACC	1 AGCCATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGGCTAT 	19 19	
1321 GTGGGANTGJAGGCCGTGCCAATTGTGATGCTCCTTGATCGTGACTGAGGAGCTGCAA	1 GGGTCACTTTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTA 	19	
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1321 GTGGGANTGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCACTGAILLILLILLILLILLILLILLILLILLILLILLILLILL	01 CCCTTTGGAATGAAGGGTACATCATGGGTTTCATCAGCAAGGAGCGGGAGCGGGCCATC 	18	
1321 GTGGGANT-GAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGAGCTGCAC	41 GCTTCTCCTTCTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTG	17 17	
1321 GTGGGANT-GAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGAGCTGCACTGAGGACTGCAGGATTGTGATGCTGACTGA	81 ACTACTCAGGGTGTCAGATCACATGGGCTAAATTCTGCAAAGAAAACATGGCTGGC	16 16	
1321 GTGGGANTGGAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGAGCTGCACCAAGCCTGCACTGAGAGTGCACTGAGAGCTGCACTGAGAGACTGCACCACCAAGCCTGCCACCAAGCCTCCTTGATCGTGACTGAGAGCTGCACCACCAAGTTGTGATGCTCCTTGATCGTGACCTAGAGACCTGCACCACCAAGTTGTGATGCCTCCTTGATCGTGACCTAGAGACCTGCACCACCAAGTTGTGATCGCACCTAGAGACCCACCACCAAGCCTCCAAGATTGACCTTGAAGACCCACCAAGCCCACCAAGGCCTCAAGATTGACCTTGAGACCCCACCACCAAGCCCCAAGACCCTAGAGACCCCACCAAGCCCCAAGACCCTAGAGACCCCAAGCCCCAAGACCCTAGAGACCCCAACCTTCCGAGACCCCAACTCTGCCAAATGCTTGCCAAGTTGACCTTAGCCACCACCAATCATCTTTCACCAAGTTGTGTGATCCTCCAACACCCCAAATCCTTGCAAATCCTTGCCAAGTTGTTGTGTGATCCTCAACCACCAAATCCTTGCAAATCCTTGCCAAGTTGTTGAACATCTTCACCTAAGCCGCCAATACCCCAAGAATACCACCAAATACCTTGCAAATACATCTTTGCAACATTCTTCACCTAAGCCGCCAATACCACCAAATACACATCTTGCAACAATACATCATTAAACAATACCACAAATACAAATACAATACAAATACAATACAAATACAATACAAATACAAATACAATACAAATACAAATACAAATACAAATACAAATACAAATACAAATACAAAAAA	1 GAGGGCTGAGCATCGAGCAGCTGACAACGCTGGCTGAGAAGCTCCTAGGGCCTGGTGTG 	16 16	
1321 GTGGGANT-GAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGAGCTGCACTGAGGACTGCACTGAGGACTGCACTGAGGACTGCACTGAGGACTGCACTGAGGACTGCACTGATGCATGTGATCGTGATCGTGACTGAGGACTGCACTGAGGACTGCACCTAGAGACTGCACCTAGAGACTGCACCTAGAGACCCCACTGAGGATTGACCTCCAGAGACTGCACCACGAGGCCTCAAGATTGACCTAGAGACCCCACTGAGATTGACCTTCAGAGACTGCACCACGAGGCCTCAAGATTGACCTAGAGACCCCACTGAGACTCCACAATCAAT	1 TTGGAACCTGGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCACCAGCAAG 	15	
1321 GTGGGANTGJAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCAC	1 TGTGGTATAACATGCTGACCAATAACCCCAAGAACGTGAACTTCTTCACTAAGCCGCCA 	15	
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1321 GTGGSANTSJAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCAC 	1 TGATCACCTTCCAGACTGAGGTGTACCACCAAGACCCTAAAATTGACCTAGAGACCCAC 	13	
	1 GTGGGAAFGJAGGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCAC 	13	

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APPLICANT: Karras, James G.
TITLE OF INVENTION: Antisense Oligonucleotide Modernic OF INVENTION: Expression
FILE REFERENCE: ISPH-0338
CURRENT APPLICATION NUMBER: US/09/288,461
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 82
LENGTH: 2869
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FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (69)...(2381)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: U06922
DATABASE ENTRY DATE: 1994-07-01
US-09-288-461-82
                                                                                                              Query Ma
Best Loc
Matches
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GENERAL INFORMATION:
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TGCACCAGCTGTACAGCGACACGTTCCCCATGGAGCTGCGGCAGTTCCTGGCACCTTGGA
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                                       GCAGCAGGATGGCTCAGTGGAACCAGCTGCAGCAGCTGGACACACGCTACCTGAAGCAGC
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                                                                                           GCCGCGACCAGCCAGGCCGGCCAGTCGGGCTCAGCCCGGAGACAGTCGAGACCCCCTGACT
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                             gcagcaggatggctcagtggaaccagctgcagcagctggacacacgctacctgaagcagc
                                                                                Application
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                                                                                                               Score 2864.2;
Pred. No. 0;
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APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF A
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application Patent No. 6235873
                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/364,970 CURRENT FILING DATE: 1999-07-31 NUMBER OF SEO ID NOS: 10
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1200	tgaattatcagcttaaaattaaagtgtgcattgataaagactctggggatgttgctgcc	1	Дb
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US-08-416-581B-7
REFERENCE/DOCKET NUMBER: 0-37:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08416581B Patent No. 5719042
                                                                                                                         COMPUTER READABLE FORM:

MEDJUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTI
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                                                                                          APPLICATION NUMBER: JP 6-65825/1994 FILING DATE: 04-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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STREET: 21
CITY: Wash
STATE: D.C
COUNTRY: U
ZIP: 20037
                                                                     NAME: Nakamura, Dean REGISTRATION NUMBER:
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Best Local Similarity
Matches 2436; Conserv
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TYPE: nucleic acid
TYPANDEDNESS: single
TOPOLOGY: linear
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                   CCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCCGCCAACAAAT 910
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                   CACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTAGAGCCATACAC
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FILING DATE: 04 APR-1994 FILING DATE: 04 APR-1994 ATTORNEY/AGENT INFORMATION: NAME: NAKAMURA, Dean H. REGISTRATION NUMBER: 33,981 REFERENCE/DOCKET NUMBER: 0-37891 TELECOMMUNICATION INFORMATION: TELEPAX: (202)293-7860 TELEFAX: (202)293-7860 TELEFAX: (202)293-7860 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 2652 base pairs TYPE: nucleic acid STRANDEDNESS: Single TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA	CATION NUMBER: US/08/41 DATE: 04-APR-195 GRADABLE FORM: R READABLE FORM: R TYPE: FlopPy disk M TYPE: FlopPy disk TER: IBM PC compatible PC-DOS/MS-APE: PatentIn Release # APPLICATION DATA: CATION NUMBER: US/08/41 DATE: 04-APR-1995 IFICATION: 435 IFICATION DATA:	T 11 -416-581B-8 -416-581B-8 uence 8, Application US/08416581B ent No. 5719042 ent No. 5719042 APPLICANT: Kishimoto, Tadamitsu APPLICANT: Akira, Shizuo APPLICANT: TRANSCRIPTION FACTOR APRF AUDRESPONDENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W. CITY: Washington	GACCTCGGAGTGTGCTACCTCCCCCATGTGAGGAGCTGAAACCAGAAGCTGCAGAGACGT 2410	ATTGACCTGCGATGTCCCCCCCCCCCCTTTAGATTCATTGATTG		CAAGUAGCAGCIGAACAACAIGICAITIGCIGAAAICAICAIGGCIAIAAGAICAIGGA 2240 TGCGACCAACATCCTGGTGTCTCCACTTGTCTACCTCTACCCCGACATTCCCAAGGAGGA 2110

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Matches 2436; Conserv
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ORGANISM: Mous
TISSUE TYPE: L
FEATURE:
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                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-65825/1994
FILING DATE: 04-APR-1994
APTORNET/AGENT INFORMATION:
NAME: NAKAMURA, DEAN H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: 0-37891
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7060
TELEFAX: (202)293-7060
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARRATERISTICS:
IFNORTH: 2310 has a Dairs
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GENERAL INFORMATION:
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CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2037
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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: LENGTH: 2787 base pa

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA to

US-08-416-581B-3
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US-08-416-581B-3
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Patent No. 571904
                                                                                        Matches
                                                                                                      Query Match
Best Local
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APPLICANT: Kishimoto, Tao
APPLICANT: Akira, Shizuo
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416
FILING DATE: 04-APR-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UP 6-6582
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 0-37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2021)93-7660
                                                                                                                                                                                                                                                                         TELEFAX: (202)293-7860 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION,
STREET: 2100 Pennsylvania
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NUMBER OF SEQUENCES:
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STREET: 2100 Penns
CITY: Washington
STATE: D.C.
COUNTRY: HEAA
ZIP: 2003/
121
                              213
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGACCTCGGAGTGTGCTACCTCCCCCATG 2378
                           GGTGAAGGTGCTGAGCCCTCAGCAGGAGGGCAGTTTGAGTCGCTCACGTTTGACATGGAT
TGCACCAGCTGTACAGCGACACGTTCCCCCATGGAGCTGCGGCAGTTCCCTGGCACCTTGGA 180
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                                                                                                     Similarity
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                                                                                                                                                                                                                                          2787 base pairs
                                                                                        Conservative
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04-APR-1995
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                                                                                                     Score 2144.2;
Pred. No. 0;
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                                                                                        Mismatches
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CATTCTGGGCACGAACACAAAAGTGATGAACATGGAGG 126	TCAGAGGGTCTCGGAAATTTAAG	1201	Qy
AGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCC 12 	TGAATTATCAGCTTAAAATTAAAG	1141 1293	Оy
TACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGT 11 	TCATCAAGACTGGTGTCCAGTTT	1081 1233	Qy Db
GCAGCCCTGCATGCCCATGCACCGGACCGGCCCTTAG 10 	AGAGTGCCTTCGTGGTGGAGCGGC	1021 1173	Qу
GGAGGAGAGGATCGTGGAGCTGTTCAGAAACTTAATGA 10 	TCGTGCAGCACCGGCCCATGCTGG	961 1113	DЪ
GGAGCTGCAGCAGAAAGTGTCCTACAAGGGCGACCCTA 96	GCCAACAAATTAAGAAACTGGAGG	901 1053	Дb
CTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCC 90	TCTGCCTGGACCGTCTGGAAAACT	841 993	Оy
GCGGCCAGAGATCGCGTGCATCGGAGGCCCTCCCAACA 840 	AAGAGCTGGCTGACTGGAAGAGGC	781 933	Qy Db
GTCAC GTCAC	TGAGTGAGCTGCGGGGGCTCTTGT	721 873	Qy Db
GATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTG 720 	AGAAGATGCAGCAGCTGGAACAGA 	661 813	Оу
GCAGGATCTGAATGGAAACAACCAGTCTGTGACCAGAC 660 	CCCTCAAGAGCCAAGGAGACATGC	601 753	Qy
GGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAA 600 	TAGAACAGAAAATGAAGGTGGTGG	541 693	Оу
GCAGCATCTTCAGGATGTCCGGAAGCGAGTGCAGGATC 540 	CAGAGAAGCAGCAGATGTTGGAGC	481 633	Оу
AGGGGGCCAGGCCAACCACCCAACAGCCGCCGTAGTGA 480 	CGGCAGCCACGGCAGCAAG CTGCAGCCACTGCGGCCCAGCAAG	421 573	Оу
GGCCCGATGCCTGTGGGAAGAGTCTCGCCTCCTCCAGA 420 	CAATGGAAATTGCCCGGATCGTGG	361 513	ОУ
AATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGC 360 ATCAAGCAGTTTCTTCAGAGCAGGTATCTTGAGAAGC 512	TCTATCAGCACAACCTTCGAAGAAT	301 453	Оу
CCAGCAATATAGCCGATTCCTGCAAGAGTCCAATGTCC 300 	ATAATCTCTTGGGTGAAATTGACCA	241 393	Оy
IGCAGCCAGCAAAGAGTCACATGCCACGTTGGTGTTTC 240 	TTGAGAGTCAAGACTGGGCATATGC	181 333	Оу
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Length

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US-08-416-581B-4
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-08-416-581B-4
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                         TELEFAX: (202)293-7860 / INFORMATION FOR SEQ ID NO: // SEQUENCE CHARACTERISTICS: LENGTH: 2787 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 6-
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
                                         FEATURE:
                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
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CITY: Washington
STATE: D.C.
COUNTRY: USA
21P: 20037
            NAME/KEY:
LOCATION:
                                                        ORGANISM: HC
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                                                         Homo sapiens
E: Placenta
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100 Pennsylvania Avenue, N.W.
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Best Local Similarity
Matches 2305; Conserv
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                                                                                                                      CCCTCAAGAGCCAAGGAGATGCAGGATCTGAATGGAAACAACCAGTCTGTGACCAGAC
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TCATCAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGT
                 TTGTACAGCACCGGCCGATGCTGGAGGAGGAGCATCGTGGAGCTGTTCAGAAACTTAATGA
                                                            TCGTGCAGCACCGGCCCATGCTGGAGGAGGATCGTGGAGCTGTTCAGAAACTTAATGA 1020
                                                                                      GTCAACAAATTAAGAAACTGGAGGAGTTGCACCAAAAAGTTTCCTACAAAGGGGACCCCA
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Pred. No. 0;
0; Mismatches
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Sequence 1, Application US/09288461
Patent NO. 6159694
GENERAL INFORMATION:
APPLICANT: Karras, James G.
TITLE OF INVENTION: Antisense Oligonucleotide Mod
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0338
CURRENT APPLICATION NUMBER: US/09/288,461
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 107
SOCTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2787
TYPE: DNA
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Best Local Similarity 90.9
...-^hes 2305; Conservative
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LOCATION: (221)...(2533)
PUBLICATION INFORMATION:
JOURNAL: Cell
VOLUME: 77
                                                                                                                                ISSUE: 1
PAGES: 63-71
PAGES: 63-71
DATE: 1994-04-08
DATABASE ACCESSION NUMBER: L29277
DATABASE ENTRY DATE: 1994-12-31
-09-288-461-1
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Pred. No. 0;
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1260	TCAGAGGGTCTCGGAAATTTAACATTCTGGGCACGAACACAAAAGTGATGAACATGGAGG	1201	Оy
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120	TGAATTATCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGGATGTTGCTGCCC	1141	Qу
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1140 1292	TCATCAAGACTGGTGTCCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGT	1081 1233	Оу
108	AGAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCATGCACCCGGACCGGCCCT1AG	1021	Qу
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780	TACGTGCAGAAGACACTGACTGATG	721	Qy
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720	GACCAGATGCGGAGAAGCATTG	661	Оy
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600	AGGTGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAA	541	Qу
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480	CAGCAAGGGGGCCAGGCCAACCACCCAACAGCCGCCGTAGTGA	421	Qу
632		573	
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572		513	Db
360 512	TCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGC 		Qу
300	CCAGCAATATAGCCGATTCCTGCAAGAGTCCAATGTCC	241	Qу
452		393	
240	TTGAGAGTCAAGACTGGGCATATGCAGCCAGCAAGAGTCACATGCCACGTTGGTGTTTC	181	Qу
392		333	

Search completed: March 19, 2002, 15:19:34 Job time: 4716 sec

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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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H6112360 60290049
H6976226 602846477
AK018544 Mus muscu
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BI108275
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ALIGNMENTS

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM JOURNAL COMMENT RESULT 1
BI156115
LOCUS
DEFINITION FEATURES source National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Henrighausen Ph.D., Chu-Xia Deng Ph.D.
cDWA Library Preparation: Life Technologies, Inc.
cDWA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
CDWa distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM/11092 row: P. Column: 19 mRNA sequence. BI156115 BI155115 947 bp mRNA 602903680F1 NIH_CGAP_Mam3 Mus EST BI156115.1 GI:14616116 asnow esnot e: LLAM11092 row: p column: quality sequence stop: 772. Location/Qualifiers : Eutheria; 1 to 947) a; Metazoa; Chordata;
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/clone="IMAGE:5033346"
/clone_lib="NIH_CGAP_Mam3" /tissue_type="tumor, gross tissue" /lab_host="DH10B" 947 bp Mus Craniata; certebrata; Euteleostomi, Sciurognathi: Muridae; Murinae; Mus musculus ci)NA clone 05-JUL-2001 IMAGE:5033346 Mus. .

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BASE COUNT
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TGTGCTACC-TCCCCCATGTGAGGAGCTGAAACCAGAAGCTGCAGAGACGTGACTTGAGA 2419
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                                              CAAGCAGGGAGGCCAAGTTGAAGTCGGCTCACGTTTTGACATTGGATCTGACCTCGGAGG
                                                                        CAGGAGGGCAGTTTGAGTCGCTCACGTTTGAC----
                                                                                                                                                                   CCAAGTTCATCTGTGTGACACCAACGACCTGCAGCAATACCATTGACCTGCCGATGTCCC
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                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
plate: LLAM10910 row: h column: 15
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone=lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="nfiltrating d
/dev_stage="5 months"
/lab_host="DH10B"
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Site_2: Not1; Cloned unidirectionally. primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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/strain="FVB/N"
/db_xref="taxon:10090"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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602795715F1 NIH_CGAP_Mam4 Mus
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                   http://image.llnl.gov
Plate: LLAM10827 row: n column:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                            CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
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                      quality sequence start: 2 quality sequence stop: 781. Location/Qualifiers
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CCATCCTAAGCACAAAAGCCCCCGGGCACCTTCCTAATGGGCTTCAG-GAGAGCAGCAAG
                                         CCATCCTAAGCAC-AAAGCCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAA 1913
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/lab_host="PHIUB"
/lab_host="PHIUB"
/lab_host="PHIUB"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: pCMV-SPORT6; Site_1: Not1;
/note="Org
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/clone="IMAGE:4916931"
/clone_lib="NIH_CGAP_Mam4"
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TITLE
JOURNAL
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Best Local
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                                                                1905 AGCAGCAAAGAAGGAGGGGTCACTTTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACC
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  1965 CAGATCCAGTCTGTAGAGCCATACACCAAGCAGCTGAACAACATGTCATTTGCTGAA 2024
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B1156246
B1156246.1 G1:14616247
EST.
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plate: LLAM11092 row: c column: 04
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert 2 kb. Library constructed by Life
Technologies, catalog #12017-018. Investigators providing
samples: Lothar Hennighausen/Chu-xia Deng, NII Reference
for transgenic model: Xu et al., Nature Genetics 22, 37-43
(1999). Note: this is a NCI_CGAP Library."
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/lab_host="DH10B"
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90.0%;
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b 269	CAGATCCAGTCTGTAGAGCCATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAA 328
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)b 329	ATCATCATGGGCTATAAGATCATGGATGCGACCAACATCCTGGTGTCTCCACTTGTCT
λу 2085	TCTAC
ъ 389	CTCTACCCCGACATTCCCAAGGAGGAGGCATTTGGAAAGTACTGTAGGCCCGAGAGGC
2y 2145 2b 449	GAGCACCCCGAAGCCGACCCAGGTAGTGCTGCCCCGTACCTGAAGACCAAGGTTCATCTGT 2204
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ეხ 506	GTGACACC
6	TCATTGATGCAGTTTGGAAATAACGGTGAAGGTGCTGAGGCCTCAGCAGGAGGGCAGTTT 23
)b 566	TCATTGATGCAG-TTGGAAATAACGGTGAAGGTGCTGAGCCCTCAG
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ob 685	GCTGAAACCAGAAGCTGCAGAGACGTGACTTGAGACACCTGCCCCCTGCTCCACCCCTAA 744
Ωу 2445	GCAGCCGAACCCCATATCGTCTGAAACTCC
Db 745	GCAGCCGAACCCCATATCGTCTGAAAACTCCTTAACTTTTGTGGTTCA
2y 2502 Db 805	TTAATTTCCTAC-TTCTGCTATCTTTGGGCAATCTGGGCACTTTTTAAAAGAGAGAAA 2558
2y 2559	TGAGTGAGTGT-GGGTGATAAACTGTTATGTAAAGAGGAGAGA
Db 865	- TGAGTTGCTGTGGGGTGCGATACACTGTTCCTGGTCACGGAGGAGGAGCCCTCTGA
Ωу 2618	GGGGCTGAGAGCAGAAAGGGGAA
Db 925	GGGATGGGGCTTGAAACCGAGGACCCCCGGGAACCCTCCTGGTCTGGCGGCCTGGCC
267	TTTTTCAGCAG 26
286 90	
RESULT 5 BG975502 LOCUS DEFINITION	BG975502 602842871F1
ACCESSION VERSION KEYWORDS	mKNA sequence BG975592 BG975502.1 G EST. house mouse.
ORGANI	Ma De de Ma Ma
AUTHORS	1 (bases 1 to 840) NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.
	rement: Lothar Hennighausen Ph.D., P
	cDNA Library Preparation: Life Technologies, Inc.

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                                                                                                                                                                                                                           CAGCAATACCATTGACCTGCCGATGTCCCCCCCCCCCACTTAGATTCATTGATGCAGTTTTGG
                                                                                                                                                                                                                                                                                 CCCAGGTAGTGCTGCCCCGTACCTGAAGACCAAGTTCATCTGTGTGACACCAACGACCTG
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Plate: LLAM10975 row: m column: 18
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/clone_lib="NIH_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/lab_host-"DH10B"
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/db_xref="taxon:10090"
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Matches 723;
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               959 TATCGTG VGCACCCVGCCCATGCTGGAGGAGAGGATCGTGGAGCTGTTCAGAAACTTAAT 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Plate: LLAM10916 row: n column: 03
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National Institutes of Health, Mammalian
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a 183 c 198 g 158 t 1 others
                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type-"infiltrating
/dev_stage="5 months"
/lab_host="DH10B"
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                                                                                                                                                                                                                                 mRNA sequence.
BG174177
BG174177.1 GI
                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Glibert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
I (bases 1 to 869)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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602334170F1 NCI_CGAP_Mam1 Mu:
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                                                                                                                                                                                                             house mouse
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CAGAAACTTAATGAAGAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCCATGCACCC
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/clone="IMAGE:4457248"
/clone=lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
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Pred. No. 4.1e-152;
0; Mismatches 18;
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                   GCAAGACCCAGATCCAGTCTGTAGAGCCATACACCAAGCAGCAGCTGAACAACATGTCAT
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                                                       TCAGCGAGAGCAGCAAAGAAGGAGGGGTCACTTTCACTTGGGTGGAAAAGGACATCAGTG
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BG175965 889 bp mRNA 602337885F1 NCI_CGAP_Mam1 Mus musculus mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 889)
NIH-MGC http://mgc.nci.nih.gov/.
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BG175965.1 GI:12682668
EST.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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/clone_lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
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96.9%;
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Pred. No. 7.8e-151;
0; Mismatches 19;
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, A
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602900049F1 NCI_CGAP_Mam5 Mu:
                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11083 row: b column: 13
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                         quality sequence stop:
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="1MAGE:5029548"
                                                                                          Location/Qualifiers
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clone IMAGE:5029548
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/clone_lib="NCI_CGAP_Mam5"

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ACCAACGAGCCTGCAGGCAATACCCATTGACCTGCCGATTGTCCCCCCCGGC
                                                  TGTAGAGCCATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAAATCATCATGGG
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                                                                               CCGAAGCCGACCCAGGTAGTGCTGCCCCGTACCTGAAGACCAA--GTTCATCTGTGTGAC
                                                                                                         TGTAGAGCCATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGG
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                        ACCAACGACC---TGCAGCAATACCATTGACCTGCCGATGTCCCCCCGCAC 2257
                                                                                                                                    ACATTCCCAAGGAGGAGGCATTT - - GGAAAGTACTGTA - GGCCCGAGAGCCAGGAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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            CCAGTTTACCACGAAAGTCAGGTTGCTGGTCAAATTTCCTGAGTTGAATTATCAGCTTAA
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Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/sex="female, virgin"
/tissue_type="infiltrating d
/dev_stage="5 months"
/lab_host="DH10B"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo o
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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/db_xref="taxon:10090"
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                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yunda, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Riken integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome research. 10 (11), 1757-1771 (2000)
Nature 409,
5 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 2634)
           Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                         FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new common research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 2634)
Carninci, P., Shibata, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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                                                                           (bases 1 to 2634)
e RIKEN Genome Exploration
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Sciurognathi;
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mouse cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide (10-JUL-20
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EPDFHAVEPYTKKELSAVTFPDIIRNYKVMAAENIPENPLKYLYPNIDKDHALGKYYS
RPKEAPEPMELDDPKRTGYIKTELISVSEVHPSRLQTTDNLLPMSPEEFDEMSRIVGP
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ELLNSIELTONTLINDELVEMKROGSACIGGPNACLDQLOSMTIVAETLOOIROO
LKKLEELEQKETYEDDPITKHKOVLSORTFILLFOOLIOSSFVVEROPOMPTHPOPRIV
LKTGYOFTVKLRLLVKLOELNYNLKVKVSFDKDVNEKNTVKGFRKFNILGTHTKVMNM
EESTNGSLAAEFRILOKLOELNYNLKVKVSFDKDVNEKNTVKGFRKFNILGTHTKVMNM
EESTNGSLAAEFRILOKEOKNAGNRTNEGPLIFELHSLSFETGLCOPGLVIDLET
TSLPVVVISNVSOLPSGMASILMVNLVTEPRRLTFFLHDPCAMMSQLSEVLSWOFSS
TSLLVVVISNVSOLPSGMASILMVNLVTEPRRLTFFLHDFCAMMSQLSEVLSWOFSS
VTKRCLNADOLSMLGEKLLGPNAGPDGLIPMTRFCKENINDKNFSFWPWIDTILELIK
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HAAYDVSFATIRFHDLLSQLDDQYSRFSLENNFLLQHNIRKSKRNLQDNFQEDPVQMS
MITYNCLKEERKILENAQRFNQAQEGNIQNTVMLDKQKELDSKVRNVKDQVMCIEQEI
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/db_xref="mGD:mGI:103063"
/db_xref="mGD:mGI:1907734"
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/strain="C57BL/6J"
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Query Match Best Local Similarity

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CTCGTGGAGTGGAAGCGAAGGCAGCAGAGCGCCTGCATCGGGGGACCGCCCAACGCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCAGCAGCTGGAACAGATGCTCACAGCCCTGGACCAGATGCGGAGAAGCATTGTGAGT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGAAATCAAGACCCTAGAAGAATTACAAGATGAATATGACTTTAAATGCAAAACCTCT
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                                                                                                                                                                                                                       CTGGATCAGCTGCAAAGCTGGTTCACCATTGTTGCAGAGACCCTGCAGCAGATCCGTCAG 1126
                                                                                                                                                                                                                                      CTGGACCGTCTGGAAAACTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCGCCAA 905
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                                                                                                                                                                                                                                                                                                                                                             GCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCCCATGCACCCGGACCGGCCCCTTAGTCATC 1085
                                                                                                            AAAAACAAGCAGGTGTTGTCAGATCGAACCTTCCTCCTCTTCCAGCAGCTCATTCAGAGC 1246
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	318 AAAGACCACGCCCTTGGGAAGTATTAT 2344	Db 2	U
	- H	Ν	Qγ
2317		N	D
2102	043 ATCATGGATGCGACCAACATCCTGGTGTCTCCACTTGTCTACCTCTACCCCGACATTCCC	2	γQ
2257	198 CCCTACACGAAAAAGAACTTTCAGCTGTTACTTTCCCAGATATTATTCGCAACTACAAA	2	Дb
2042	CATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGGCTAT	<u> </u>	Qy
2197	AGAACGAGGTGAACCTGACTTCCATGCCGTGGAG	2	ద
1982	TTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTAGAG	_	γQ
2137		N	Дb
1925	CCCCGGCCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAAGAAGAAGGAGGGGTC	_	γQ
2077	GGAATGATGGGTGCATTATGGGCTTCATCAGCAAGGAGCGAGAACGCGCTCTGCTCAAG	2	Вb
1865	806 TGGAATGAAGGGTACATCATGGGTTTCATCAGCAAGGAGCGGGGGGGG	, 	ξO.
2017		_	DЬ
1805	746 TCCTTCTGGGTCTGGCTAGACAATATCATCGACCTTGTGAAAAAGTATATCTTGGCCCTT	<u></u>	Qy
1957		_	Д
1745	686 TCAGGGTGTCAGATCACATGGGCTAAATTCTGCAAAGAAAACATGGCTGGC		Qy
1897	1 CTGAACGCAGACCAGCTGAGCATGCTGGGAGAAGCTGCTGGGCCCTAATGCTGGC	b 18	DЬ
1685	26 CTGAGCATCGAGCAGCTGACAACGCTGGCTGAGAAGCTCCTAGGGCCTGGTGAACTAC	у 16	VΩ
1840	81 TGGTGGTCCCAGCTCTCAGAGGTGTTGAGTTGGCAGTTTTCATCAGTCACCAAGAGAGGT	b 17	В
1625	66 ACCTGGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTCGTCCACCAAGCGAGGG	у 15	γQ
1780	21 TACAACATGCTGGTGACAGAGCCCAGGAATCTCTCCTTCCT	b 17	뮵
1565		_	γQ
1720	61 CCTGTCGTGGTGATCTCCAACGTCAGCCAGCTCCCCAGTGGCTGGGCGTCTATCCTGTGG	ь 16	밁
1505	46 CCAGTTGTGGTGATCTCCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATCCTGTGG	у 14	δ
1660	01 AGCTTTGAAACCCAGTTGTGCCAGCCAGGCTTGGTGATTGACCTGGAGACCACCTCTCTT	b 16	Вb
1445	86 ACCTTCGAGACTGAGGTGTACCACCAAGGCCTCAAGATTGACCTAGAGACCCACTCCTTG	γ 13	Qy
1600	41 AACGCTGGGAACAGAACTAATGAGGGGCCTCTCATTGTCACCGAAGAACTTCACTCTCTT	o 15	В
1385	26 AATGGACGCCGTGCCAATTGTGATGCCTCCTTGATCGTGACTGAGGAGCTGCACCTGATC	/ 13	QΥ
1540	87	14	В
1325	166 AACAACGGCAGCCTGTCTGCAGAGTTCAAGCACCTGACCCTTAGGGAGCAGAGATGTGGG 1	/ 12	γQ
1486		14	В
1265	90	12	ρ
1426	67	13	ф
1205	.146 TATCAGCTTAAAATTAAAGTGTGCATTGATAAAGACTCTGGGGATGTTGCTGCCCTCAGA 1		γ

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                                                 AGAGCCATACACCAAGCAGCAGCTGAACAACATGTCATTTGCTGAAATCATCATGGGCTA 2038
                                                                                                                                              AGGGGTCACTTTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGT 1978
                                                                                                                                                                                                                                                                                                         GGCCCTTTGGAATGAAGGGTACATCATGGGTTTCATCAGCAAGGAGCGGGAGCGGGCCAT 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTAAGCACAAAGCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAAGAAGG 1918
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                                                                                                                                                                                                   CCTAAGCACAAAGCCCCCGGGCACCTTCCTACTGCGCTTCAGCGAGAGCAGCAAAGAAGG
                                                                                                                           AGGGGTCACTTCACTTGGGTGGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGT
al Similarity
695; Conserv
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11089 row: i column: 09
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Dencona Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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BI108275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: this is a NCI_CGAP Library."
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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Plate: LiAM10977 row: k column:
High quality sequence stop: 714.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2.5 kb. Library constructed by Life Technologies, catalog # 12018-016. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Liet al., Cell Growth and Differentiation 7, 3-11 (1996). Note: this is a NCI_CGAP
                                                                                                                                                                                                         /tissue_type="tumor, gross tisser"
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                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
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Query Match Best Local Similarity

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 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Den
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 736)
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BI155944.1 GI:14615957
                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                    Contact: Robert Strausberg, Ph.D.
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/tissue_type="tumor, gross tissue"
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/clone="IMAGE:5033995"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/strain="C57/B6"
/db_xref="taxon:10090"
/clone="fMAGE:5028140"
/clone_lib="NCL_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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Search completed: March 19, 2002, 14:30:29 Job time: $1772 \cdot \cdots$

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C:Species: Homo Sapiens (man)
C:Date: 21 Feb-1997 *sequence_revision 21-Feb-1
C:Accession: A54444
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.;
Cell 77, 63 71, 1994
A;Title: Molecular cloning of APRF, a novel IF1
A;Reference number: A54444; MUID:94208062
A;Accession: A54444
A;Status: preliminary; translated from GB/EMBL,
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: GB:L29277; NID:9475788; PII
C:Genetics:
A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:129277; NID:9475788; PII
C:Superfamily: human signal transducer and tran
C;Keywords: DNA binding; transcription factor
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                      TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLK
                                                                LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
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           TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLK
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                    SQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEEL
                                                                                 QLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN
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RESULT A46159

interferon-dependent positive-acting transcription (Species: Homo sapiens (man) (C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 (C;Accession: A46159 R;Schindler, C.; Fu, X.Y.; Improta, T.; Aebersold, Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992 A;Title: Proteins of transcription factor ISGF-3: 0 A;Reference number: A46159; MUID: 92366557 A;Accession: A46159 A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator A;Status: preliminary; not compared with A;Molecule type: nucleic acid; protein A;Residues: 1-739 <SCH> conceptual one R . ; #text_change 28-Jul-2000 factor gene Darnell Jr., ISGF-3 encodes 91K chain -STAT5A the J E 91-and human 84 - kDa

В Ş DЪ QΥ Matches 121 Local 61 61 MAQWNQLQOLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLK LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120 MSQWYELQQLDSKFLEQVHQLYDDSFPMEIRQYLAQWLEKQDWEHAANDVSFATIRFHDL 60 LSQLDDQYSRFSLENNFLLQHNIRKSKRNLQDNFQEDPIQMSMIIYSCLKEERKILENAQ Similarity Conservative 48.9%; Score 1971.5; DB 2; 51.7%; Pred. No. 4.7e-114; tive 144; Mismatches 189; Length 25; Gaps 60

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RESULT
A56047
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                                                                                                                                                                                                                                             A;Reference number: A56047; MUID:94277038
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence
A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
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 LGEIDQQYSRFLQESNVLYQHNLRRIKOFLQSRYLEKPMEIARIVARCLWEESRLLQTAA
                                                                               MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                                                  MSQWNQVQQLEIKFLEQVDQFYDDNFPMEIRHLLAQWIETQDWEVASNNETMATILLQNL
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                                                                                                                                                                                                                                                                                                               RESULT 5
A46160
A46160
interferon alpha-induced transcription activator ISGF-3, N;Alternate names: stat2 protein C;Speckes: Homo sapiens (man) C;Date: 21-Sep-193 #sequence revision 18-Nov-1994 #text_C;Accession: A46160: S71908; S53873
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A;Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E. Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple expns
                                                                                                                                  R; Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; submitted to the EMBL Data Library, December
                                                                                                                                                                               A;Status: preliminary: not compared with conceptual A;Molecule type: mRNA; protein A;Residues: 1-851 <fUl>
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A; Accession: S71908
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                                                                 A; Residues: 1-851 <YAN>
                                                                               A; Molecule type: DNA
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A:Reference number: $53873; MUID:95192056
A:Accession: $53873
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-196:392-591;684-730 <YAM>
A:Cross-references: EMBL:U18671
C:Genetics:
A:Genetics:
A:Gene: stat2
A:Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2: 345/2; 365/2:
C:Superfamily: human signal transducer and transcription activator STAT5A
C:Keywords: signal transduction; transcription regulation
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C; Species: Homo sapiens (man)
C; Date: 21-Dec-1996 *sequence_revision 06-Jun-1997 *text_change 28-Jul-2000
C; Accession: G02317
R; Lin, J.
R; Lin, J.
R; Lin, J.
R; Lin, J.
R; Edge number: H01043
A; Reference number: H01043
A; Accession: G02317
A; Status: preliminary; translated from GB/FMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-794 < LIN>
A; Cross-references: EMBL:043185; NID:91151169; PIDN:AAB06589.1; PID:91151170
C; Superfamily: human signal transducer and transcription activator S1AT5A
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TLDSLMQFGNNGEGAEPSAGGQFESLTFDMDLTSECA
                                                                                                                                                                                                                                                                                                                                                                                                                                 KTLSLPVVVIVHGSQDHNATATVLWDNAFA-EPGRVP-FAVPDKVLWPQLCEALNMKFKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HQA-TGTLSAHFRNMSLKRIK-----RADRRGAESVTEEKFTVLFESQFSVGSNELVFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETE--VYHQGLKIDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTTKVRLLVKFPELNYQL - - - KIKVCIDKDSGDVAALRGSRKFN - - - - ILGTNTKVMNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHLCQQLPIPG-PVEEMLAEVNATITDIISALVTSTFIIEKQP-----PQVLKTQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSAMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KTLKSQGDMQDL-----NGNNQSVTRQKMQQLEQML----TALDQMRRSIVSELAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
249; Conserv
                                                        PVLAKAVDGYVKPQIKQVVPEFVNASADAGGSSATYMDQ---
                                                                                                                                                                   SPERNLWNLKPFTTRDFSIRSLAD-----RLGD-----LSYLIYVFPDRPKDEVFSKYYT
                                                                                                                                                                                                                      SGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCR
                                                                                                                                                                                                                                                                                  MEVLKKHHKPHWNDGAILGFVNKQQAHDLLINKPDGTFLLRFSD-SEIGGITIAW--KFD
                                                                                                                                                                                                                                                                                                                                       IDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDI
                                                                                                                                                                                                                                                                                                                                                                                             EVQSNRGLTKENLVFLAQKLFNNSSSHLEDYSGLSVSWSQFNRENLPGWNYTFWQWFDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.6%; Score 869.5; DB 2 ilarity 30.5%; Pred. No. 5.9e-46; Conservative 146; Mismatches 315
                                                                                                              SQEHPE----ADP-GSAAPYLKTKFICVTPTTCSNTIDLPMSPR 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
  766
                                                        APSPAVCPQA-PYNMYPQ
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FDLDETMDVA

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Wighternate names: STAT5 protein homolog p80

C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Accession: I49274; S54773; S54727
R;Liu, X; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved A;Accession: I49273; MUID:96004632
A;Accession: I49274
A;Accession: I49274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-432,'E',434-786 <MUI>
A;Residues: 1-432,'E',434-786 <MUI>
A;Cross-references: EMBL:248539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R;Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu,
EMBO J. 14, 1402-1411, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: mRNA
A;Residues: 1-432,'E',434-786 <AZA>
C:Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54772; MUID:95237198
A;Accession: S54773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-786 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 249; Conserv
  397
                                                       348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYA----ASKESHATLV 56
                                                                                                                                                                                                                                                                                                             FHNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLL 116
EESNNGSLSAEFKHLTL----REQRCGNGGRANCDASLIVTEELHLITFETEVYHQG--L
                                                       FAATVRLLVG-GKLNVHMNPPQVKATIISEQQAKSLLKNENTRNDYSGEIL-NNCCVMEY 405
                                                                                                         FTTKVRLLVKFPELNYQL---KIKVCIDKDSGDVAALRGSRKFN----ILGTNTKVMNM 396
                                                                                                                                                                                                                                                                                                                                                                                       OESLRIQAQFAQLGOLNPQERMSRETALQQKQVSLETWLQREAQTLQQYRVELAEKHQKT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                           -KTLKSQGDMQDLNGNN-----QSVTRQKMQQLEQML----TALDQMRRSIVSELAGL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REANNGSSPAGS----LADAMSQKHLQINQTFEELRLITQDTENELKKLQQTQEYFIIQY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEGLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQSTYDRCPMELVRCIRHILYNFQRLV 120
                                                                                                                                                                 EHLCQQLPIPG-PVEEMLAEVNATITDIISALVTSTFIIEKQP-----PQVLKTQTK 347
                                                                                                                                                                                                                     EELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQ 344
                                                                                                                                                                                                                                                                             LQLLRKQQTIILDDELIQWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAMWIQAQQIQGDAI.HQMQAI.YGQHFPIEVRHYI.SQWTESQAWDSIDI.DNPQENTKATQI. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 143; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.6%; Score 868.5; DB 2; 30.2%; Pred. No. 6.8e-46; Live 143; Mismatches 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
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	Y 176	VLVDAMSQKHLQINQRFEELRLITQDTENELKKLQQTQEYFIIQY	: ::: DINQREEELRLITQUT!	TGVLVDAMSQKHLQ	REANN	121	DЬ
	Y 176	EQKMKVVENLQDDFDFNY	MLEQHLQDVKKRVQDLI	Ξ	QTAAT/	117	Qy
		MELVRCIRHILYNEQRLA				61	Db .
	L 116	MEIARIVARCLWEESRLI	LRRIKQFLQSRYLEKPI	:: NEQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARTVARCLWEESRLL	FHNL	57	Qy
	r 60 : 95	WAYAASKESHATIA 	PMELRQFLAPWIESQD : : : PIEVRHYLAQWIESQP	CLOGGDALROMYSOTFPMELROFLAPWIESQDWAYAASKESHATIV	MAQWNO: MAGW)	1 1	Db Qy
28;	Gaps	ength 793; . Indels 106; (ore 858; DB 2: ad. No. 3e-45; Mismatches 320		y Match Local Simi hes 245:	uery M est Lo latches	Z 10 O
	TAT5A	activator ST/	er and transc	∴ı signal transduce	tat' mily	perfa	C;S
	747972	. 90.1; PID:g74	:9747971; PII.	A;Rosidues:	efc.	esidue ross-r) A A :
			om GB/EMBL/DI	translated iro	֖֖֓֞֟֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	tatus:	A 2-2
b) involve	itat5	¹ homologue (cat5 and an <i>e</i> 04632	119273; MUID: 9600	Cloni ce n	itle: eferen	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
	58634	AA88419.1; PID:g758 ; Hennighausen, L.	:g758633; PIDN:C/ , F.; Groner, B. RI-8835 1995	Sci II S A 92 883	eference; Robins	ross-r	R; C
		\$ 1	sequence not show	A;Status: prelne iry; nucleic acid s A;Molecule type: ERNA A:Residnes: 1-7:: AUT>	prelume types	tatus: olecul osidne	A A; R M S
d interleu	tor and	y stimulating facto	nacrophage colony 37198	ikin-3, granulocyte-m er: S54772; MUID:9523 772	Interled ce number on: 85%	itle: eferen ccessi	A; T
		; Miyajima, Λ.)'Farrell, A.M.; Harada, N 95	, H.,)/Farrell,	L.F.; Wo	11, A.	R; M
	1 - 2000	#!vt_change 28-Jul	JI.	mammary gland factor - mouse N;Alternate names: stat5 protein C;Species: Mis musculus (house mouse) C;Date: 27-Oct-1945 isequence_revision 03-Nov-199 C:Accession: \$54,775 149,773	land facte names: Mus mu 7-Oct-1: con: 8547	mary g lterna becies ate: 2	mam C;S A
					80	JLT 772	RESULT S54772
		7	: : :	HYNMYPPNPDSVLDTDGD	- HYNNYP	(Li)	Db
		ECA 766	\GGQFESLTFDMDLTSH	IDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMDLTSECA	IDLPMSP	722	Qy
	A 737	TDAGSGATYMDQAPSPVVCPQA	TVPEFANASTDAGSGAT	CREST	KYYTDVP	681	Db V
	-	CNIETI VE PORPROEVIO	NOTE ADDOMAN	GRIDGO GEORGE AND SERVICE OF SERV	- KrusQe	000	מ
		LVSPLVYLYPDIPKEEAFG	IMGYK IMDATNI	KDISGKTQIQSVEPYTKQQI.NNMSFAEIIMGYKIMDATNII.VSPLVYI.YPDIPKEEAFG	- 8	625	. Q
			CQQAHDLLINKPLGTFI		FDGVMEV	574	DB 49
		AMAGELADOS ASSESSES I	SSNHLEDI NSMSV5W2	SNRGLENENLYF LAUKLFNI	KEKAEVO	n	2 5
	N 564	AKFCKENMAGKGESEWVN	GONNYSGCQITWA	QFSSTTKRGLSIEQLITLAEKLLGPGVNYSGCQITWAKFCKENMAGKGFSFWVW	QFSST	511	Qy
	513	AVPDKVLWPQLCEALNM	LWDNAFA - EPGRVP - F	SLPVVVIVHGSQDNNATATV	VEQVETE	456	Db
	₹ 510	TKPPIGTWDQVAEVLSW	I.WYNMLTNNPKNVNFF	KIDLETHSLEVVVISNICOMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSW	KIDLETH	451	Оу
	455	VTEEKFTILFDSQFSVGGNEL	AGSVTEE	HQA-TOTESAHERNMSEKRIKRSDRRGAGS	:: 1: HQA-1:T	406	DЬ

Query Match Best Local Similarity

19.6%; 29.3%;

Score 791.5; Pred. No. 3.9

.9e-41; DB 2;

Length

794;

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mammary gland factor - sheep
C:Species: Ovis orientalis aries, Ovis ammon
C:Date: 27-Oct-1995 #sequence_revision 03-Nc
C:Accession: S55527; 544353
R:Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A:Title: Corrigenda. Mammary gland factor (Markeference number: S55527; MUID:95188889
A:Accession: S55527
A:Cross-references: EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g602355
A:Note: this is a revision to the sequence from reference S44353
R:Makao, H: Gouilleux, F: Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regular, Reference number: S44353; MUID:94244619
A:Reference number: S44353
A:Molecule type: mRNA
A:Residues: 1-716, 'RHLHGPGSLPSR',729,'P',731,'ASL' <WAW>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S5527
C:Superfamily: human signal transducer and transcription activator STAT5A
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A; Residues: 1-794 <WAK>
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QNPDPVLD--QDGE---
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                                                                                                                                                                                                                                                                                                                                            VKTLSLPVVVIVHGSQDHNATATVLWDNAFA-EPGRVP-FAVPDKVLWPQLCEALNMKFK
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                              RTLDSLMQFGNNGEGAEPSAGGQFESLTFDMDLTSECA 766
                                                                  TPVLAKAVDGYVKPQIKQVVPEFVSASADSAGSSATYMDQ---APSPAVCPQP-HYNMYP
                                                                                                                                     DSPDRNLWNLKPFTTREGSIRSLAD-----RLGU-----LNYLIYVFPDRPKDEVFSKYY
                                                                                                                                                                                                      VMEVLKKHHKPHWNDGAILGFVNKQQAHDLLINKPDGTFLLRFSD-SEIGGITIAW--KF
                                                                                                                                                                                                                                                                           AEVQSNRGLTKENLLFLAQKLFNNSSSHLEDYNGMSVSWSQFNRENLPGWNYTFWQWFDG
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                                                                                                   -SQEHPE----AD-PGSAAPYLKTKFICVTPTTCSNTIDLPMSP
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RESULT 10
157557
DNA-Binding Protein and transcription factor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 28-Jul-2000
C:Date: 17557
C:Accession: 17557
C:Accession: 17557

R:Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, Mol. Cell. Biol. 15, 3336-3343, 1995
A;Title: Cloning of murine Stat6 and human Stat6, Stat proteins the A;Reference number: 157557; MUID:95280934

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A; Reference number: A; Accession: 157557

A; Status: preliminary; translated from GB/EMBL/DDBJ

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A;Residues: 1-837 <RES>
A;Cross references: GB:L47650;
C;Genetics:
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interleukin-4-induced transcription
C; Species: Homo sapiens (man)

factor stat -

human

676

PDSSMS-MOLG

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C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 28-Jul-2000 C;Accession: A54740 R;Hou, J; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S. Science 265, 1701-1706, 1994 A;Title: An interleukin-4-induced transcription factor: IL-4 stat. A; Reference number: A54740; MUID:94367369 A;Accession: A54740 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mSNA A
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                                                                                                                         EAFGKYCRPESQEHP----
                                                                                                                                                                                                                                  FTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKE
                                                                                                                                                                                                                                                                                                    FWQWFDGVLDLTKRCLRSYWSDRLIIGFISKQYVTSLLLNEPDGTFLLRFSD-SEIGGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQTKF@A:\vkFLLGLRFLGAPAKPPLVRADMVTEKQARELSVPQGPGAGAESTGEIINNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGLLSAMEYYQKTLTDEELADWKRRPETACTGGPPN1CLDRLENW1TSLAESQLQTRQQ1
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                                                              EAFRSHYKPEQMGKDGRGYVPATIKMTVERDQPLPTPELQM-----PTMVPSYDLGMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGEIDQQYSRFL---QESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQ
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207; Conserv
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ilarity 26.2%;
Conservative 13
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18; Pred. No. 1.6e-26;
138; Mismatches 287;
                                                                                                                      EADPGSAAPYLKTKFICVTPTTCSNTIDLPMS
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S32763; 137947
R:Kruppa, G.; Fuetterer, A.; Lemke, H.; Kroenke, M.
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A;Title: Molecular cloning and characterization of human kinectin A;Reference number: 137947; MUID:95306853
A;Accession: 137947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: Cloning and characterization of TAF, A;Reference number: $32763
A;Accession: $32763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:KTN1
A;Cross-references: GDB:6165852; OMIM:600653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1356 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1356 < KRU>
A; Cross-references: EMBL: Z22551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z22551; NID:g296163; PIDN:CAA80271.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 145; Conserv
                                                                                                                                                                                                                                                                                 RLLV-KFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTK--VMNMEESNNGSLSA 406
                                                                                                    VISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEV---LSWQFSSTTK--
                                                                                                                                                                                         EFKHLTLREQRCGNGGRANCD----ASLIVTEELHLITFETEVYHQGLKIDLETHSLPVV 462
                                                                                                                                                                                                                                       QTLVSEQPNKDVVEQMEKCIQEKDEKLKTVEELLETGLIQVATKEEELNAIRTENSSLTK
                                                                                                                                                                                                                                                                                                                            SVYVKDDKI----RLLEEQLQHEISNKMEEFKILN-----DQNKALKSEVQ---KL
                                                                                                                                                                                                                                                                                                                                                                     KVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKV 349
                                                                                                                                                                                                                                                                                                                                                                                                               QTEDSLASERDRLTSKEEELKDIQN-MNFLLKAEVQKLQALANEQAAAAHE---LEKMQQ 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTDEELADWKRK-----PEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --KEESLQMQVQDILEQNEALKAQ-IQQFHSQIAA--QTSASVLAEELHKVIAEKDKQIK 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTAATAAQQGGQANHPTAAVVTEKQ-QMLEQHLQDVRKRVQDLEQK-MKVVENLQDDFDF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLQESNVLYQHNLRRIKQF-----LQSRYLEK-----PMEIARIVARCLWEESRLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQNKIHVSYQETQQMQMKFQQVREQMEAE---IAHLKQENGILRDAVSNTTNQLESKQS- 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRKRTAEHEAAQQDLQSKFVAKENEVQSLHSKLTDTLVSKQQLEQRLMQLMESEQKRVN- 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --AELNKLRODYARLVNELTEKTGKLQQEEVQKKNAEQAATQLKVQLQEAERRWEEVQSY 502
RGLSIEQLTT---
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                -LAEKLLGPGVNYSGCQITWAKFCKENMAGKGFSFWVWLDN 567
                                                                                                                                                -DQVSFASLV--EELKKVIHEKDGKIKSVEELLEAELLKV-
                                                           -ANKEKTVQDLKQEIKALKEEIGNVQLEKAQQLSITSKVQ 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119;
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9; Mismatches
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Pred. No. 0.045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278;
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C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-2000
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-2000
C:Accession: A42184; S33376; S55331; S23647; S24554
R:Compton, D.A.; Szilak, I.; Cleveland, D.W.
J. Cell Biol. 116, 1395-1408, 1992
A:Title: Primary structure of NuMA, an intranuclear protein that detines a A:Reference number: A42184; MUID:92176238
A:Accession: A42184
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A;Map position: 11q13-11q13
C;Keywords: mitosis; nucleus
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A;Rolecule type: mRNA
A;Residues: 1-771,'Q',773-814,'ER',817-872,'E',874-1267,'KLKLLQAETASNSARAAERSSALREEVQ
A;Cross-references: EMBL:Z11583; NID:g35118; PIUN:CAA77669.1; PID:g35119
A;Cross-references: EMBL:Z11583; NID:g35118; PIUN:CAA77669.1; PID:g35119
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J. Cell Biol. 116, 1303-1317, 1992
A;Title: NuMA: an unusually long coiled-coil related
A;Reference number: S23647; MUID:92176231
A;Accession: S23647
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A; Residues: 1705-2101 <TAN>
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A:Accession: S33376
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A; Residues: 247-279 <HAR>
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ches 118;
357 EKQAQLEKELSAALQDKKCLEEKNEILQGKLSQLEEHLSQLQDNPPQEKGEVLGDVLQLE
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                                                                                                                                                               QCQDLKTEKSQMDRKINQLSEENGD-LSFKLREFASHLQQLQDALNELTEEHSKATQEWL
                                                                                                                                                                                                                                            QLQQLDT-----RYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKE-SHATLVFH 58
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22.0%;
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Pred. No. 0.17;
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A; McCess. DNA
A; McCess. A; McCess. A; McCess. A; McCess. A; McCess. A; McCess. A; Cross-references: EMBL: X81635; NID: 9550427; PID: 9550429
R; Huang, M.E.; Chu.t, J.C.; Galibert, F.
R; Huang, M.E.; Chu.t, Sequence Database, September 199
                                                                A; Reference
A; Accession:
                                                                                                                                                                                                  A;Title: RAD26, the functional S.cerevisiae A;Reference number: S50230; MUID:95045431 A;Accession: S50231
                                                                                                                                                                                                                                                                A;Residues: 1-1085 <MAN>
A;Residues: 1-1085 <MAN>
A;Cross-references: EMBL:249535; NID:g1015682; PID:g1015683; MIPS:YJR035w R;Van Gool, A.J.; Verhage, R.; Swagemakers, S.M.A.; van de Putte, P.; BrouemBO J. 13, 5361-5369, 1994
                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S57052
A; Accession: S57054
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A; Residues: 1-1085 <HUA>
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Biochem. Biophys. Res. Commun. 201, 310-317, 1994
A; Title: A possible yeast homolog of human active-gene-repairing
A; Reference number: JC2227; MUID:94256996
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable helicase RAD26 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein GTA1085; protein J1606; protein
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Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 21-Jul-2000
Accession: JC2227; S48295; S57054; S50231; S63779; JC2372
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                   S63757; MUID:95397595
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C;Keywords: DNA binding
F;173-228/Region: acidic
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A:Molecule type: DAA
A;Residues: 1-1085 <HUW>
A;Cross-references: EMBL:L36344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross - references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: SGD: RAD26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: the nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 142;
   539
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                                                          HNR111 SCIPPA----
                                                                                                                                                                                                                                                                                                     CVQWL - -
                          LNNMS YELLMGYKIMDATNILVSPLVY-----LYPDIPKEEAFGKYCR 688
                                                                                                                                              QITWAKFCKENMAGKGFSFWVWLDN1IDLVKKYILALWNEGYIM----GFIS-----KE
                                                                                                                                                                                                                                                                    EVYHQGI.KIDLETHSLPVVVISNIC-----
                                                                                                                                                                                                                                                                                                                                                                                                                     KILKELEDLR----FRGQPGEAKDDGDELYYQERLKKWVKQRSCCSQRSSULPEWRRP--
YANATTI DVQTGYKCAVALRDLISPYLLRRVKADVAKDLPQKKEMVLFCK
                                                                                     RERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKD--ISGKT-----QIQSVEPYTKQQ 644
                                                                                                                     RIHSDKLLK-----
                                                                                                                                                                               ENLIMNSKPSDFSYE
                                                                                                                                                                                                        KNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGL-SIEQLTTLAEKILGPG----VNYSGC 542
                                                                                                                                                                                                                                     ALHHSGLLTGPVLTVCPATVMKQWCNEFQHWWPPLRTVILHSM\;SGMASDQKFKMDENDL
                                                                                                                                                                                                                                                                                                                                 NTKVM
                                                                                                                                                                                                                                                                                                                                                                                       PMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGT
                                                                                                                                                                                                                                                                                                                                                                                                                                               --IKKLEELQQKVSYKGDP-----IVQHRPMLEERIVELFRNLMKSAFVVE-RQPCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAMEYVQKTLTDEE--LADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPTAAVVTEKQQMLEQHLQDVRKRVQ--DLEQKMKVVENLQUDFDFNYKTLKSQGDMQDL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVLYQHNLKR-----IKQFLQSKYLEKPMEIARIVARCLWEESKLLQTAATAAQQGGQAN 130
                                                                                                                                                                                                                                                                                                                                                                -- HDV:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - ATEQMVENLTDEDDNLSD - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt NKGSKEGLQRPGETEKEFLIRTGKITAFGHKAGFSLDTANREYAKNDEQKDEDFEM----}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLTRKLNNTTRISVKQNLRDQIKNIQSDDIERVLKDI----DDIQSRIKELKEQVDQGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVLSQSSLEEKIANDVTNFSNLQSLQQ------EETRLERSKTALQRYVNKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 105;
                                                                                                                                                                                                                                                                                                                              SNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHL-----ITFET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.98;
                                                                                                                                                                                                                                                                                                -YELYQQNCGG----
                                                                                                                                                                            -DWKNSTRTKKALESSYHLDKLIUKVVTDGHILITTYVGL
                                                       - IQNNLTELWSLFDFIFPGKLGTLPVFQQQFVIPINIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not shown;
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                                                                                                                  ----VKWQYAVLDEGHKIRNPDSEISLTCKKLKT 490
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No. 0.071;
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CG1 protein - human C;Species: Homo saplens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000 C;Accession: 15379; R;Print, C.G.; Leung, E.; Harrison, J.E.; Watson, J.D.; Krissansen, G.W.

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Gene 144, 221-228, 1994
A;Title: Cloning of a gene encoding a human leukocyte protein characterised by extensive A;Title: Cloning of a gene encoding a human leukocyte protein characterised by extensive A;Reference number: I53799
A;Accession: I53799
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1300 <RES>
A;Cross-references: GB:L25616; NID:g409465; PIDN:AAB65853.1; PID:g409466
C;Genetics:
A;Cross-references: GB:L25616; NID:g409465; PIDN:AAB65853.1; PID:g409466
A;Cross-references: GDB:C31
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                                                 EKDISGKTQ-IQSVEPYTK-----QQLNNMSFAE 652
                                                                                             LQEENESLKAHVQEVAQHNLKEASSASQFEELEIVLKEKENELKRLEAMLKER-----
                                                                                                                                         I---IDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWV 624
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ESDLSSKTQLLQDVQDENKLFKSQIEQLKQQNYQQ 987
                                                                                                                                                                                        ELONLLKGKE-EOMNTMKAVLEEK------EKDLANTG----KWLQD 899
                                                                                                                                                                                                                -----RGLSIEQLTT----LAEKLLGPGVNYSGCQITWAKFCKENWAGKGFSFWVWLDN 567
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                                                                                                                                                                                                                                                                                                                                                                      EVQDLKAKQN------DQVSFASLV--EELKKVIHEKDGKIKSVEELLEAELLKV- 824
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Search completed: March 19, 2002, 15:23:41 Job time: 368 sec

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Result
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-08-948-547-12
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ALIGNMENTS

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TOPOLOGY. Finear : MOLECULE TYPE: protein US-08-369-796-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: James E.
                                                        INFORMATION SEQ ID NO: SEQUENCE ("AAACTERISTICS: LENGTH: ") amino acid
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LUM PO compatible
COMPUTER: LUM PO compatible
OPERATIN: SYSTEM: PC-DOS/MS-DOS
SOFTWARF Patentin Release #1.0, Version #1.75
CURRENT WITON DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Curt M. Horvath
APPLICANT: Chong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
                                                                                                                                                                                            TELECOMM:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Zilong Wen
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CITY: Hackensack
STATE: New Jerse
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"NUMBER: 26,742
"NUMBER: 600-1-116

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Query Match 100.0%; Score 4029; Best Local Similarity 100.0%; Pred. No. 0; Matches 770; Conservative 0; Mismatches

DB 1; 0;

Length 770;

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RESULT 2
US-08-852-091-12
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                                                                                                                                                                                     TITLE OF INVENTION: FÜNCTIONALLY ACTIVE REGIONS OF SIGNAL TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                     APPLICANT: James E. Darnell,
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                             ADDRESSEE: Klauber
STREET: 411 Hackens
CITY: Hackensack
STATE: New Jersey
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Best Local S
Matches 770
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FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
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CLASSI-ICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                  GCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST
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                                                                   ; MOLECULE TYPE: US-08-820-754-12
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-193
ATTORNEY/AGENT INFORMATION:
APPLICATION TOWNER: US 08/126,588
FILING DATE: 24-SEP-193
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
PEFERENCE/DOCKET NUMBER: 600-1-073 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Klauber & Jackson
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19-MAR-1997
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   100.0%;
 Score 4029;
Pred. No. 0;
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                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Durnell Jr., James E.

APPLICANT: Schindler, Christian

APPLICANT: Fu, Xian Yuan

APPLICANT: Wen, Zilong

APPLICANT: Wen, Zilong

APPLICANT: Zhong, Zhong
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
STREET: 411 Hackensac
CITY: Hackensack
STATE: New Jersey
                                                                                 APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPPGTIILKFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQI.NNMSFAEIIMGYKIM
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                                     E: Klauber & Jackson 411 Hackensack Avenue
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Best Local Similarity
Matches 770; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 23-NOV-1992
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
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MEDIUM TYPE:
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PRIOR APPLICATION DATA:
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/212,185 FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
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              QLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN 420
                                                           HRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNY
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)GY: linear
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100.0%; Pred. No. 0;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/212,185

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/854,296

FILING DATE: 19-MAR-1992

PRIOR APPLICATION NUMBER: WO US93/02569

FILING DATE: 19-MAR-1993

PRIOR APPLICATION NUMBER: WO US93/02569

FILING DATE: 19-MAR-1993

PRIOR APPLICATION NUMBER: US 08/126,588

APPLICATION NUMBER: US 08/126,588

FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-073 CITELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Klauber & Jacks
STREET: 411 Hackensack Ave
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatibl
OPERATING SYSTEM: PC LOSS/W
SOFTWARE: Patentin Release
CURRENT APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION COMPANIED CONTROL
OPERATION: 
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APPLICANT: Schindler, Cl
APPLICANT: Fu, Xian-Yua
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
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Schindler, Christian
Fu, Xian-Yuan
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SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TYPE: linear
HOLECULE TYPE: protein
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TELEX: 133521
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           TIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMDLTSECATSPM 770
                                                                               NMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYS
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TIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMDLTSECATSPM
                                                  DATNILVSPLVYLYPDIPKFEAFGKYCRPFSOEHPEADPGSAAPYLKTKFICVTPTTCSN 720
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RESULT 6
US 0.0-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:

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PRIOR APPLICATION NUMBER: US/08/
APPLICATION NUMBER: US/08/
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
APPLICATION NUMBER: US 07/
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US9
FILING LATE: 19-MAR-1993
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,54
FILING DATE:
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APPLICATION NUMBER: 1
FILING DATE: 24-SEP-
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CORRESPONDENCE ADDRESS:
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APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIL
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
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NAME: Jackson Esq., Davi
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CITY: Hackensack
STATE: New Jerse
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APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS.

TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 3
10 NO 370
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                                                                                                                                                            LENGTH: 770
TYPE: PRT
ORGANISM: Mus n
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TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLK 180
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                                                                                                         Conservative
                                                                                                                                                                      musculus
                                                                                                                  100.0%;
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                                                                                                                   Score 4029;
Pred. No. 0;
                                                                                                          Mismatches
                                                                                                                              DB 4;
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APPLICATION NUMBER: PFILING DATE: 28-DEC-1
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0

UMBER: PCT/US95/17025 28-DEC-1995

Version

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GENERAL INFOHMATION:
GENERAL INFOHMATION:
APPLICANT: James E. Darnell
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
STREET: ...! Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-TOSS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
COURT OF THE CONTROL OF THE CON
                                                                                                                                                                                                                                                                       TITLE OF INVENTION: FÜNCTIONALLY ACTIVE REGIONS
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF
NUMBER OF SIQUENCES: 39
CORRESPONDENTE ADDRESS:
ADDRESST: Klauber & Jackson
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TRANSCRIPTION (STAT) PROTEINS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
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CLASSIFICATION:
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            TIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMDLTSECATSPM 770
                                                DATNILVSPLYYLYPDIPKEEAFGKYCRPESOEHPEADPGSAAPYLKTKFICVTPTTCSN 720
                                                                                                    KPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIM
                                                                                                                                                        GCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST
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                                                                                    KPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIM
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DATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN
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US-09-012-710-8
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US-09-012-710-8
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APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Moarefi, Jr., James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-
TITLE OF INVENTION: STAT PROTEIN AND ME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-343-1684
TELEX: 1 731
INFORMATION 104 SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7/0 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
TELEX: 7.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATE: NUMBER: 26,742
REFERENCE/PACKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Klauber
STREET: 411 Hackens
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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CLASSIFICATION:
                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino a
                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                       1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
SQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLL.SAMEYVQKTLTDEEL
                                                                                                                                      TAAQQGGQANHPTAAVVTEKQOMLEQHLQDVRKRVQDI.EQKMKVVENLQDDFDFNYKTLK 180
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                                                           SQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEEL
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411 Hackensack Avenue,
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GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEO ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 5
LENGTH: 770
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; Patent No. 6235873
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US-09-364-970-5
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Best Local Similarity
Matches 768; Conserv
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TYPE: PRT
ORGANISM: Mus musculus
-09-364-970-5
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99.7%;
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Pred No. 0;
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GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu APPLICANT: Akira, Shizuo TITLE OF INVENTION: TRANSCRIPTION
APPLICATION NUMBER: US/08/416
EILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-6582
FILING DATE: 04-APR-1994
ATTORNEY_AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: 0-37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, M
STREET: 2100 Pennsylv
CITY: Washington
STATE: D.C.
                                                                                                                                                                             COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 11
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                                                                                                                                                                  US/08/416,581B
                                                                                                         6-65825/1994
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US-08-416-581B-9
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INFORMATION FOR SEO ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local
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Local Similarity 99.4%;
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                                                                                                                                        DATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720
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                                   US/08416581B
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Pred. No. 0;
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FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-6582
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NAKAMURA; Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: 0-37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEPAX: (202)293-7060
TELEFAX: (202)293-7060
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 759; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein 3-416-5818-1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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STREET: 2100 Penn:
CITY: Washington
STATE: D.C.
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GGRANCID.SILIVTEELHLITFETEVYHQGI.KIDLETHSLPVVVISNICQMPNAWASILWY
                                   SQGDES ANGNNQSVTROKMQOLEQMLTALDQMRRSIVSELA JAJSAMEYVQKTLIDEEL
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Pred. No. 0;
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RESULT 13
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                                      Ouery Match
Best Local Similarity 98.0
Matches 759; Conservative
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                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 6-65825/1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NAKAMUFA, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: 0-37891
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                           TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDINI TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                         TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                               SEQUENCE CHARACTERISTICS: LENGTH: 770 amino acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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APPLICANT: Akira, Shizuo
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MAQWNOLQOLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
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2100 Pennsylvania
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                                                      Score 3977;
Pred. No. 0;
                                           Mismatches
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                                                   APPLICANT: Vinkemeier, Uwe
APPLICANT: Chen, Xiaomin
APPLICANT: Chen, Xiaomin
APPLICANT: Marnell Jr., James E
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE CORE POR
TITLE OF INVENTION: USE
FILE REFERENCE: 600-1-229
CURRENT APPLICATION NUMBER: US/09/087,465A
CURRENT FILING DATE: 1998-05-29
NUMBER OF SEO ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 6
LENGTH: 770
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                 ; ORGANISM: Homo sapiens US-09-087-465-6
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                                                                                                                                                                                                                                     Sequence 6, Application US/09087465A Patent No. 616(1019)2
GENERAL INFORMATION:
                                            TYPE: PRT
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RESULT 15
US-08-276-099A-14
                                                                                                                  Sequence 14, Application US/08276099A Patent No. 5591825
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Best Local S
Matches 759
                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MCKNIGht, Steven L
APPLICANT: HOU, JINZHAO
TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS
TITLE OF INVENTION: BINDING ASSAYS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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San Francisco
California
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                                FLEHR,
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                     HOHBACH, TEST, ALBRITTON
dero Center, Suite 3400
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Pred. No. 0;
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; MOLECULE TYPE:
US-08-276-099A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, Richard Aron

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 4-59451-1/RAO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEPHONE: (415) 398-3249

TELEFAX: (415) 398-3249

TELEFX: 910 27729

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 759
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ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                   481
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
                                                                                            QLKINY...IJKDSGDVAALRGSRKFNIIJGTNTKVMNMEESNNGSI.SAEFKHLTLREQRCGN
                                                                                                                                                                              HRPMLEERTVELERNLMKSAEVVERQPCMPMHPDRPLVIKTGVQETTKVRLLVKEPELNY
                                                                                                                                                                                                                       GCQ1TWAKFCKENMAGKGFSFWVWLDN1IDLVKKY1LALWNEGY1MGF1SKERERA11.ST
                                                                                                                                                                                                                                                                  TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLK
                                                                                                                                                                                                                                                                                                                                                      LGEIDGGYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA
                                                                                                                                                                                                                                                                                                                                                                 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA
           GCQITWANFCKENMAGKGFSYWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST
                                                 NMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLS1EQLTTLAEKILGPGVNYS
                                                                                                                                       QLKIKVClokDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN
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: 15-JUL-1994
ON: 435
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98.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 3977;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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ch com	721	721	661	661	601	601
Search completed: March 19, 2002, 15:22:45 Job time: 3132 sec	721 TIDLPMSPRALDSLMQFGNNGEGAEPSAGGQFESLTFDMELTSECATSPM 770	721 TIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMDLTSECATSPM 770	661 DATNILLSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720	661 DATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720	601 KPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIM 660	601 KPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIM 660

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Minimum DB
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Copyright (c) 1993 - 2000 Com
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AAY03768
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AAR72078
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AAW03176
AAB12377
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Lung cancer associ
Human signal trans
Human placenta acu
Mouse Stat3 protei
Human Stat91. Hom
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1049	1094	1142	1146	1157.5	1167	1168	1172	1212	1290	1293	1293	1293	1293	1293	1388	1648	1714	1716	1780.5	1786	1798	~1	ı n	971	1984	1984	1984	1997	1997	1997	2017	0	2017
26.0	27.2	•		28.7	٠	٠	29.1		32.0	32.1	32.1	32.1	32.1		34.5		•	42.6	44.2	44.3			48.3		•	49.2	9.	9.	9.	9	0	50.1	50.1
376	213	223	229	228	229	229	229	236	252	851	851	851	851	851	271	582	748	748	749	704	748	748	701	739	749	749	749	712	712	712	786	750	750
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Mouse Statl protei	Mouse Stat3 protei	Mouse Stat3 protei	Mouse Stat3 mutant	Mouse Stat3 mutant	Mouse Stat3 mutant	Mouse Stat3 mutant	Mouse Stat3 protei	Stat3	Mouse Stat3 protei	Human signal trans	N-terminal domain	٠	Recognition factor	113 kD ISGF-3alpha	Mouse Stat3 protei	Human truncated St	Mouse Stat4 (13sfl	Mouse STAT3. Mus	N-terminal domain	Signal transducer	Human signal trans	Signal transducer	ISGF-		N-terminal domain		Mouse Stat1 (Stat9	Stat1-beta	STAT1-bet	Human Stat84. Hom	pancrea	Human signal trans	Human Statl-alpha

ALIGNMENTS

RESULT AAR72082

4.

AAR72082 standard; Protein;

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Mouse Stat 3 (19sf6).

27-SEP-1995 AAR72082;

(first

entry)

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24-SEP-1993;
24-SEP-1993;
11-MAR-1994;
11-MAR-1994;
                                                                                                                                                           Signal transducer and activator of transcription; STAT; 19sf6; Stat3; receptor recognition factor; transcription factor; callular debilitation; derangement; dysfunction;
N-PSDB; A 184340
      WPI; 1995 139598/18
                     Darnell JE,
                                                                                                                       W09508629-A
                                                                                                                                      Mus sp
                                    (UYRQ ) UNIV
                                                                                         26-SEP-1994;
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                                                                                                                                                      interferon-damma
                      Schindler CW,
                                    ROCKEFELLER
                                                   93US-0126588.
93US-0126595.
94US-0212184.
94US-0212185.
                                                                                         94WO-US10849
                     Shuai K,
                      Wen
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                     Zhong
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STAT1-alpha

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AAC89338) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interfer gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AAC89339-40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor recognition factor implicate stimulation of genes - useful in drufter treating cellular debilitations,
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KPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIM
                                                                                                                                                                              NMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYS
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                                                                                                                                                                                                                                                                       hrpmleerivel frnlmks \texttt{a} fvverqpcmpmhpdrplviktgvqfttkvrllvkfpelny
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  - useful in drug
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Pred. No. 0;
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Matches 770
                                                                                                                                                            followed by nuclear translocation and DNA binding to activate transcription. Recombinant STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from splanic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW03167) capable of both receptor recognition and message delivery via DNA binding in a receptor-ligand specific manner. STAT proteins and their DNA binding domains (see also AAW03165-75) are useful for screening antagonists used to inhibit STAT-mediated signal transduction
                                                                                                                                                                                                                                                                                                                              New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Domain
                                                                                                                             Sequence
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DNA binding
                                                                                                                                                                                                                                                         Mouse signal transducer and activator of transcription (STAT protein STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from ligand-activated receptor kinase complexes
                                                                                                                                                                                                                                                                                                        Disclosure; Page 87-90;
                                                                                                                                                                                                                                                                                                                                                                                                                Darnell JE,
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                                  MAQWNQLQQLDTKYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
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                      maqwnqlqqldtrylkqlhqlysdtfpmelrqflapwiesqdwayaaskeshatlvfhnl
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disease; antagonist; therapy.
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                 Location/Qualifiers
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12.21
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19.21
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28.33
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Similarity

99.7%; 99.7%;

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Length

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The present invention relates to a crystal of an N-terminal frayment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal.
                                                                                                                                                                                                                         WPI;
                                                                                                                                                      Disclosure;
                                                                                                                                                                                     New crystals of an N-terminal fragment of a activator of transcription that effectively
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QLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN
                    TAAQOGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDEDFNYKTLK 180
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The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (II-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe. ARRF-inhibitors, e.g. antibodies, antisense oligonucleotides or ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary hypertension, etc.
                                                                                                                                                                                                                                                                                                                                                                             Mouse; acute phase response factor; transcription factor; interleukin-6; signal transmission; liver; antibody; antisense; ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
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                                                                                                                                     New acute phase response factor - for developing for treating diseases induced by cytokine(s) such inflammatory diseases
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Signal Transducer and intracellular transcri

ucer and Activator of Transcription 3; transcription factor; interleukin-6; r

medicament; STAT3; allele; Human 11-JUN-1999 AAY03768 AAY03768

STAT3

allelic variant

(first

entry)

standard;

Protein;

770

AA

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Query Match 99.4
Best Local Similarity 99.4
Matches 765; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNVKTLK
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       associated proteins represented in AAB58106 - AAB5848 Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous othe diagnostic or research purposes. The proteins may be used to treat
                                                                                                                                                                                                                 Lung cancer associated gene sequences, referred antigens, useful for treatment, prevention, and
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                                                                                                                                                                             Claim
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Query Match
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                                                                                  STAT dimer. The core portion comprises a coiled-coil domain comprising 4 long helices, a DNA binding domain which contains an immunoglobulin-like fold, a C-terminal SH2 domain and a domain that links the DNA binding and SH2 domains. The crystal is of sufficient quality to perform x-ray crystallography studies. Methods of preparing the crystalls are included in the invention. Knowledge of the STAT protein's 3-dimensional structure will aid in structure-based drug design. The crystal can be used in drug screening assays to identify agonist and antagonist compounds. Antagonists can be used to treat inflammation, allergy, asthma and leukaemia, and agonists to treat anaemia, neutropenia, thrombocytopenia, cancer, obesity, viral diseases, growth retardation, and other conditions characterized by insufficient STAT activity.
                                                                                                                                                                                                                                                 The present sequence is that of human signal transducer and activator of transcription 3 (STAT). The invention provides a crystal of a core portion of a STAT protein in dimer form with an 18-mer duplex DNA (see AAAB9233) that contains a binding site for the
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                                                                                                                                                                                                                                                                                                                Column 67-71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.5%;
98.4%;
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6; Mismatches
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Matches 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is mouse Stat3 protein fragment containing 378-770 amino acids of Stat3 protein. This Stat3 fragment showed very weak binding to c-Jun protein in the cell extract.

The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, DNA binding domain, linker domain, SH2 domain and transformation, linker domain, SH2 domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying an agent transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse
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Pred. No. 3.5e-172;
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24-SEP-1993;
11-MAR-1994;
11-MAR-1994;
                                           The sequences of cDNA encoding receptor regonition factors having mol.wt. of 113 kDa (Stat113), 91 kDa (Stat92) and 84 kDa (Stat84) are given in AAQ89335-37 and the deduced amino acid sequences of STAT proteins in AAR72077-79. These ISGF-3-derived proteins are activated by binding of interferon-alpha (all 3 Stat proteins) on interferon-gamma (Stat91) to cell receptors.
                                                                                                                                                                                                                                                                Receptor recognition factor implicate stimulation of genes - useful in drifor treating cellular debilitations, dysfunctions, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal transducer and activator of transcription; ISGF-3; STAT; Stat91; receptor recognition factor; transcription factor; cellular debilitation; derangement; dysfunction; interferon-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72078 standard; Protein; 750
Sequence
                                                                                                                                                                                                                  Disclosure; Page 84-88; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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Query Match Best Local

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g oncogenesis, inllammation, parasitic disease or autoimmunity
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    New Stat protein and
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Best Local Similarity
Matches 389; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plus cysteine residue alkylation to prevent aggregation, coupled to a chromatography protocol, has allowed the purification of activated Stat proteins. The Stat proteins and fragments can be used to identify antagonists and agonists of Stat function. Antagonists can be used to treat e.g. inflammation, allergy, asthma and leukaemias, and agonists can be used in the treatment of e.g. anaemias, neutropaenias, thrombocytopenia, cancer, obesity, viral diseases, growth retardation or other diseases characterised by insufficient Stat activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is human Statl-alpha protein. The invention describes methods of producing milligram quantities of 3 forms of purified Statl protein: Statl-alpha and Statl-beta (see AAW62995) from baculovirus-infected insect cells, and Statlic (see AAW62996) from E. coli. Statl-alpha has an N-terminal compact domain that enhances the DNA binding of the Stat protein. The Tyr-701 residue is phosphorylated in vivo. In vitro phosphorylation of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is human Statl-alpha process.
of producing milligram quantities
protein: Statl-alpha and Statl-bes
protein: and Statl-bes
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                 KPPGTFLLRFSESSKEGGVTFTWVEKDIS-GKTQIOSVEPYTKQQLNNMSFAEIIMGYKI
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Pred. No. 1.2e-165;
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       The present sequence is that of human signal transducer and activator of transcription 1 (STAT-1). The invention provides a crystal of a core portion of a STAT-protein in dimer form with an C crystal of a core portion of a STAT protein in dimer form with an C la-mer duplex DNA (see AAA89233) that contains a binding site for the STAT dimer. The core portion comprises a coiled-coil domain comprising 4 long-helices, a DNA binding domain which contains an immunoglobulin-like fold, a C-terminal SH2 domain and a domain that links the DNA binding and SH2 domains. The crystal is of sufficient quality to perform X-ray crystallography studies. Methods of preparing the crystals are included in the invention. Knowledge of the STAT protein's 3-dimensional structure will aid in structure-based carug design. The crystal can be used in drug screening assays to identify agonist and antagonist compounds. Antagonists can be used to treat inflammation, allergy, asthma and leukaemia, and agonists
                                                                                                                                                                                            Claim 1; Column 41-44; 206pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human signal transducer and activator of transcription STAT-1.
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700..70
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  neutropenia,
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Human pancreatic 09-MAR-2001 AAB54098

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Agonists and antagonists to the antigens can be screened for The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, imune system, muscular, and the proteins can be used to treat or prevent neural.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gynaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynuclectide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to
                                                                                                                                                                                                                                                                                                                                                                     reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
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                                                                                                                                                                                                                                                                                                                                      Sequence
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rfng--aqsgniqstvmldkqkeldskvrnvkdkvmcieheiksledlqdeydfkcktl-
                                    TAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLK 180
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11-MAR-1994;
11-MAR-1994;
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                     Darnell
                                          (UYRQ )
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hypothetical prote
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Best Local Similarity 99.6
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Result No.

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Run 8

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accessory gene reg	A32357	s	228	٥	7	л
hypothetical prote	н83753	2	233	0.9	7	
hypothetical prote	S72930	N	232	0.9	7	ω
hypothetical prote	T32772	ν	229	0.9	7	2
hypothetical prote	T27840	2	229	0.9	7	_
C-8 sterol isomera	S33457	N	221	0.9	7	0
hypothetical prote	C84383	2	220	0.9	7	Ψ
hypothetical prote	B64168	ν	209	0.9	7	ω
mitotic feedback c	G01942	2	205	0.9	7	7
hypothetical prote	H84745	N	202	0.9	7	51
hypothetical prote	D70396	N	185	0.9	7	U
hypothetical prote	B64373	-	170	0.9	7	**
hypothetical prote	S58818	N	163	0.9	7	ω
cell division cont	S47549	Ŋ	161	0.9	7	2
signal recognition	S34196	N	136	0.9	7	_
Alu RNA-binding pr	A56062	ν	136	0.9	7	٥

ISGF3 p91-related transcription factor - mouse (;Species: Mus musculus (house mouse) (;Species: Mus musculus (house mouse) (;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000 (;Accession: 149508; 149009 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mkNA
A;Residues: 1-993', M',395-700.702-770 <RE2>
A;Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890 A;Title: Acute phase response factor and additional members A;Reference number: 149009; MUID:95014185 A;Accession: 149009 A;Cross-references: GB:L29278; NID:g476715; PIDN:AAA37254.1; PID:g476716 R;Raz, R.; Durbin, J.E.; Levy, D.E. J. Biol. Chem. 269, 24391-24395, 1994 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule typ^ mRNA A;Residues: 1-7/J <RES> A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related A;Reference number: A54444; MUID:94208062 A;Accession: I49508 $\Lambda_{\it f}$ Cene: APRF C; Superfamily: human signal transducer and transcription activator STAT5A WITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVER MLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLEN QHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQ QHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQ MLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLEN Mismatches Score 442; Pred. No. 0; DB 2; Length 770 Indels of the interferon-stimula 0; T.; Yoshida, Gaps 325 265 85 85 265 205 205 325 0;

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C:Species: Homo Saplens (man)
C:Species: None Saplens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 28-Jul-2000
C:Accession: A54444
R:Akira, S: Nishio, Y: Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; (cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related A;Reference number: A54444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: A54444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecula type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: GB:L29277; NID:9475788; PID:9475789
C:Genetics:
A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:350950
A;Map position: 17q21-17q21
C:Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor
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                    QHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQ
                                       OHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YHQGLKIDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVA
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                                                                                                             IKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQOMLE
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                                                                                           IKQFLQSRYLEKPMETARIVARCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLE
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Pred. No.
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                                                                                   C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
C;Accession: S63679
R;Suglyama, T; Nishio, Y; Kishimoto, T; Akira, S.
FEBS Lett. 381, 191-194, 1996
                                 A; Title: Identification of alternative splicing A; Reference number: $63679; MUID: 96176320 A; Accession: $63679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Accession: So 680 R:Sugiyama, T.; Nishio, Y.; Kishimoto, T.; Akira FEBS Lett. 381, 191-194, 1996 A:Title: Identification of alternative splicing A:Reference number: S63679; MUID:96176320 A:Accession: S63680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal transducer and activator of transcription 2 type c - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 02-Sep-2000
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S63680
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C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994
C:Accession: A46159
R:Schindler, C.; Fu, X.Y.; Improta, T.; Aebersold, Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A:Title: Proteins of transcription factor ISGF-3: C
 A;Status: preliminary; nucleic A;Molecule type: mRNA
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A;Experimental source: HeLa cells
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A46159
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A; Residues: 1-57 <SUG>
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type:
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1 Similarity 100.0%;
12; Conservative
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11; Conser
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Pred. No.
                sequence not shown; not compared
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0.0013;
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02-Sep-2000

with

conceptual

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Gaps

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A; Molecule type: DNA
A; Residues: 1-851 < YAN>
A; Residues: 1-851 < YAN>
A; Residues: 1-851 < YAN>
A; Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1;
R; Yan, R; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
Nucleic Acids Res. 23, 459-463, 1995
A; Title: The genomic structure of the STAT genes: multiple exons
A; Reference number: $53873; MUID:95192056
A; Accession: $53873
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-196; 392-591; 684-730 < YAN>
                                                                                                                                                                                                                                                               A:Note: sequence extracted from NCBI backbone (NCBID:110820) R:Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E. submitted to the EMBL Data Library, December 1994 A:Reference number: S71908 A:Accession: S71908
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Fu, X.Y.; Schindler, C.; Improta, T.; Aebersold, R.; Darnell Jr., Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transparence number: A46160; MUID:92366558
A;Accession: A46160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Residues: 1-748 <YAM>
A;Cross references: GB:U09351; NID:g509502; PIDN:AAA19692.1; PID:g509503
C;Superfamily: human signal transducer and transcription activator STAT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 28-Jul-2000
C;Accession: A56047
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A;Cross-references: GB:S81491; NID:g1478435; PIDN:AAB36225.1; PID:g1478436
C;Superfamily: human signal transducer and transcription activator STAT5A
                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA; protein A;Residues: 1-851 <FU1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000
C:Accession: A46160; S71908; S53873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interferon alpha-induced transcription activator ISGF-3, 113K chain - human N.Alternate names: stat2 protein
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A;Accession: A56047
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Best Local Similarity
Watches 11; Conserv
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ilarity 100.0%;
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A; Introns: 20/1
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A;Gene: stat2
A;Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2: 3
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: signal transduction; transcription regulation
                                                                                                                                                                                                                                                      R;Kershaw, J.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z20164
A;Accession: T26170
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                           C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26170
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-44 <WIL>
A;Cross-references: EMBL;AL023842; PIDN:CAA19514.1; GSPDB:GN00023; CESP:Y44A6D.1
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                                                                                                                                                              A; Experimental source: C; Genetics:
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                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-72 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein W04G5.3 - Caenorhabditis elegans
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Best Local Similarity
Matches 9; Conser
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Score 9; DB 2;
Pred. No. 0.22;
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Pred. No.
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A;Cross-references: EMBL:X63112; NID:g3968; PIDN:CAA44826.1; PID:g3970 R;Purnelle, B.; Goffeau, A. submitted to the EMBL Data Library, February 1996 A;Description: Nucleotide sequence analysis of a 40 kb segment on the right arm of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNE1 protein - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein O6353; protein YOR350c
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000
C;Accession: S67259; S67262; S20175; S67404; S19073
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C; Superfamily: F
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Nature 406, 477-483, 2000
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82180
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                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-219 <LEE>
                                                                                                                                                                                                                                     Nucleic Acids Res. 20, 449-457, 1992
A;Title: The MRE4 gene encodes a novel protein kinase
A;Reference number: S20174; MUID:92158649
                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:275258; NID:g1420761; PID:g1420762; MIPS:YOR350c A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S67261
A; Accession: S67262
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R; Delius, H.; Hebling, U.; Hofmann, B.
submitted to the Protein Sequence Database, July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-663 <GOF>
A; Cross-references: EMBL: 275258; NID: g1420761; PID: g1420762; MIPS: YOR350c
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A; Accession: S67259
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A; Molecule type: DNA
A; Residues: 1-293 <HEI>
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A; Accession: G82180
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A; Reference number: S67392
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                                                                                                                                                                                                                                                                                                                  S.H.; Ogawa,
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8; Conser
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Pred. No.
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           R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; EMBO J. 14, Il66-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony A;Reference number: S54772; MUID:95237198
A;Accession: S54773
                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 02-Unl-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Accession: 149274; S54773; S54727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involve A;Reference number: 149274
A;Accession: 149274
A;Accession: 149274
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                           A;Cross-references: EMBL:U21110: NID:g747973; P1DN:AAC52282.1; PID:g747974 R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-786 < RES>
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N; Alternate names: STAT5 protein homolog p80

mouse

preliminary; nucleic acid sequence not

stimulating

factor and interleu

mammary gland factor -

I49274

653 ELAGLLSA 660

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R.Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G. Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: Saccharomyces cerevisiae MNE1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X95720; NID:g1199839; PID:g1199852 C;Genetics:
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A; Molecule type: DNA
A; Residues: 1-663 < PUR>
                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84279
                                                                                                                                   A;Gene:
                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-728 <STO>
                                                                                                                                                                                                                                                 A; Reference number: A; Accession: F84279
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                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species:
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                                                     Query Match
Best Local
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220 ELAGLLSA 227
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                                    Similarity
8; Conser
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                                      Conservative
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                                    1.0%; Score 8; DB
100.0%; Pred. No. 19
tive 0; Mismatches
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.G.; Ja
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RESULT 15
G02317
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N;Alternate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 28-Jul-2000
C;Accession: S54772; 149273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54772; MUID:95237198
submitted to the EMBL Data Library, December 1995 A; Reference number: {\rm H01043}
                                                                               transcription activator stat5A - human C;Species: Homo sapiens (man) C;Date: 21-Dec.1996 #sequence_revision 06-Jun-1997 #text_change 28-Jul-2000 C;Accession: G02317
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C;Superfamily:
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R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved
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A:Rosidues: 1-432, E; 434-786 <MUI>
A:Residues: 1-432, E; 434-786 <MUI>
A:Residues: 1-432, E; 434-786 <MUI>
A:Residues: 1-402, 48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R:Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris, EMBO J. 14, 1402-141, 1995
A:Title: Interleukin-3 signals through multiple isoforms of Stat5.
A:Reference number: S54725; MUID:95246733
A:Accession: S54727
                                                               R; Lin, J.
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C;Genetics:
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A; Residues: 1-793 < RES>
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A:Accession: I49273
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A;Molecule type: mRNA
A;Residues: 1-432,'E',434-786 <AZA>
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A; Residues: 1-793 <MUI>
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Best Local Similarity
Matches 8; Conserv
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ilarity 100.0%;
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100.0%; Pred. No. 20;
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Pred. No.
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A:Accession: G02 > /
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: EMBL:043185: NID:gl151169; PIDN:AAB06589.1; PID:gl151170
C:Superfamily: human signal transducer and transcription activator STAT5A
C:Superfamily: human signal transducer and transcription activator STAT5A
Ouery Match
Best Local Similarity 100.0%: Score 8; DB 2; Length 794;
Best Local Similarity 100.0%: Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy 604 GTFLLRES 611
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Db 613 GTFLLRES 6.11
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Search completed: March 19, Job time: 193 Search

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TISSUE-KIDNEY A
Strausberg R.;
Strausberg |
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SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3.
                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                           Q9BW54
                                                      NCBI_TaxID=9606;
                                                                            Homo sapiens (Human)
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 BC000627;
ENCE 769 A
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                                                               Chordata;
Primates;
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                                                               Craniata; Vertebrata;
Catarrhini; Hominidae
 A374A32AB9D28077
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 CRC64;
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Best Local
Xenopus laevis (African clawed Eukaryota; Metazoa; Chordata; C Amphibia; Batrachia; Anura; Mes Xenopodinae; Xenopus. NCBI_TaxID-8355; [1]
                                  O9PVX8
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                                              ) (TrEMBLrel. 13, 10) (TrEMBLrel. 13, 11) (TrEMBLrel. 17,
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Last sequence u
Last annotation
                  Mesobatrachia;
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Pred. No. 3e-262; 
4; Mismatches
                        Craniata;
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                              frog)
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Interpro; IPR001217; STAT
Interpro; IPR001217; STAT
Pfam; PF00017; STAT; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE: PS50001; SH2; 1.
PROSITE: PS50001; SH2; 1.
SEQUENCE 769 AA; 87974
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"Activation of Stat3 by cytokine embryos independently of BMP-4.";
Dev. Biol. 0:0-0(1999).
EMBL; AB017701; BAA86061.1; -.
HSSP; P42227; 1BG1.
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Nishinakamura R., Matsumoto Y.,
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Best I
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O93599
O1-NOV-1998 (TrEMBLrel. 0
O1-NOV-1998 (TrEMBLrel. 0
O1-NOV-1998 (TrEMBLrel. 0
O1-JUN-2001 (TrEMBLrel. 1
TRANSCRIPTION FACTOR.
STAT3.
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Interpro: IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00255; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 806 AA; 92151 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Merazoa; Chordata; Craniata; Vetebrata; E
Actinopterydii, Meopterygii, Teleostei, Euteleostei;
Cypriniformes; ('yprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                     Oates A.C.;
Thesis (1998), University o
EMBL; AJ005693; CAA06677.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Local :
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NYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRC
                                                                                                                          ELADWKRRQQIACIGGPPNICLDRLETWITSLAESQLQIRQQIRKLEELQQKVSYKGDPI
                                                                                                                                                                ELADWKRRPEIACIGGPPNICLDRLENWITSLAESOLQTRQQIKKLEELQQKVSYKGDPI
                                                                                                                                                                                                                                                                                   MAQWNQLQQLETRYLEQLYHLYSDSFPMELRQFLAPWIESQNWAYAANKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                   678;
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                  Conservative
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85.1%;
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                                                                                                                                                                                                                                                                                                                 Score 3474; DB 13;
Pred. No. 3.8e-227;
43; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence up
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Best L
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InterPro; IPR001217; STAT.
Pfam; PP00017; STAT; 1.
Pfam; PF01017; STAT; 1.
SEQUENCE 767 AA; 87816 M
                                                                                                                                                                                                                                                                                                                                                                                             013133;
013133;
01-JUL-1997
01-JUL-1997
01-JUN-2001
                                                                                                                                                                                                                                                                                   Johnson M.C., Mourich D.V
Submitted (JUN-1996) to th
EMBL; U60333; AAB60926.1;
HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                           Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa: Chordata; Craniata; Petrebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei;
Pertacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8022;
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                                                               SLTLDMELSSDHA-SPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLTFDMDLTSECATSPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMDATNILVSPLVYLYPDIPKEEAFGKYCRPEA--HPDTEFPDTGCVTQPYLKTKFICVT
IQHRPALEEKIVDLFRNLMKSAFVVERQRCMPMHPDRPLVIKTGVQFTNKVRLLVKFPEL
                                                                                                                                                                                                    656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEA---DPGSAA-PYLKTKFICVT
                                                                                                                                   LGEIDQQYSRFLQENNVLYQHNLRRIKQHLQSKYLEKPMEIARIVARCLWEEQRLLQTAT
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 04, Created)
(TrEMBLrel. 04, Last sequence up
(TrEMBLrel. 17, Last annotation
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                            83.7%;
                                                                                                                                                                                                                                                                                                     D.V.,
                                                                                                                                                                                                                                            MW.
                                                                                                                                                                                                    53;
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                           Score 3373.5;
Pred. No. 2.36
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Matches 396
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InterPro; IPR001217; STAT.
Pfam; PP00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 749 AA; 87234 MW; 1
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O9OXKO;
O1-MAY-2000 (Trembi
O1-MAY-2000 (Trembi
O1-JUN-2001 (Trembi
SIGNAL TRANSDUCER A
STAT1.
                                                                                                                                                                                                                                                            Chen G., Newgard C.B.;
"Expression of STATI in INS-1 cells.";
Submitted (NOV-1999) to the EMHL/GenBa
EMBL; AF205604; AAF20200.1; -.
HSSP; P42224; 1BF5.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
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                                                                                   NYQLKIKYCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRC
                                                     LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WYNMLTNHPKNVNFFTKPPVGTWDQVAEVLSWQFSSTTKRGLTIEQLTTLAEKLLGPCVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WYNMLTNNPKNVNFFTKPPJGTWDQVAEVLSWQFSSTTKRGLS1EQ1.TT1.AEKLI.GPGVN
 RFNQAQEGNIQN---
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                   --TAAQQGGQANHPTAAVVTEKQQMI.EQHLQDVKKRVQDI.EQKMKVVENLQDDFDFNYKT 178
                                          LSQLDDQYSRFSLENNFLLQHNIRKSKRNLQDNFQEDPVQMSMIIHNCLKEERKILENAQ
                                                                                                                              tch 50.6%; al Similarity 51.8%; 396; Conservative 14
                                                                                                                                                                                                                                                                                                                                                                                                         ("TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence of (TrEMBLrel. 17, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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AND ACTIVATOR OF TRANSCRIPTION 1.
TVMLDKQKELDSKVRNVKDQVMCIEHEIKTLEDLQDEYDFKCKT
                                                                                                                              %; Score 2038; DB 1
%; Pred. No. 7e-130;
145; Mismatches 19
                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                                                                  DB 11;
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; Murinae; Rat
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RESULT
OPD323
OPD 323

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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Ra Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Ra Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Nikaido I., Pesole G., Quackenbush J., Radota M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Raka K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Raka K., Okido T., Bojunga N., Carninci P., de Bonaldo M.F., Rabake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Rabakinotich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., And Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Na Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09D323;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=COLON;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Rodentia;
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Sciurognathi; Muridae; Murinae; Mus.
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InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 749 AA; 87280 M
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EMBL; AK018544; BAB31265.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
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VHPSRLQTTDNLLPMSPEEFDEMSRI - -
                                                                          KIMDATNILVSPLVYLYPDIPKEEAFGK-YCRP-ESQEHPEADPGSAAPYLKTKFICVT-
                                                                                                                      MAQWNQLQOLDTRYLKQLHQLYSDTFFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                   STKPPGTFLLRFSESSKEGGVTFTWVEKDIS-GKTQIQSVEPYTKQQLNNMSFAEIIMGY
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                 --PTTCSNTID-LPMSPRTLDSLMQFGNNGEGAEPSAGGQFESL
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144; Mismatches
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION
Mus musculus (Mouse).
Bukbryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae
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Submilted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC004808; AAH04808.1; -.
SEQUENCE 712 AA; 83106 MW; D62081709638CDA5 CRC64;
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                                                                                                                   LSQLDDQYSRFSLENNFLLQHNIRKSKRNLQDNFQEDPVQMSMIIYNCLKEERKILENAQ 120
KVMAAENIPENPLKYLYPNIDKDHAFGKYYSRPKEAPEPMELDDPKRTGYIKTELISVS
           KIMDATNILVSPLVYLYPDIPKEEAFGK-YCRP-ESQEHPEADPGSAAPYLKTKFICVT
                                                                                       TKNKQVLSDRTFLLFQQLIQSSFVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQEL
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                                                                            PDGL-IPWTRFCKENINDKNFSFWPWIDTILELIKKHLLCLWNDGCIMGFISKERERALL
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385; Conser
                                                                                                                                                                                                                                                                                                                     SQNREGEANGVAKSDQKQEQLLHKMFLMLDNKRKEIIHKIRELLNSIELTQNTLIND
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No. 9.7e-128;
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Matches 380
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O13131;
O1-JUL-1997 (TrEMBLrel. 04, C:
O1-JUL-1997 (TrEMBLrel. 17, L:
O1-JUN-2001 (TrEMBLrel. 17, L:
SIGNAL TRANSDUCER/ACTIVATOR O)
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InterPro; IPR001217; STAT:
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 754 AA; 86872 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson M.C., Mourich D.V., submitted (JUN-1996) to the EMBL; U60331; AAB60924.1; -. HSSP; P42224; 1BF5.
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                                                                                                                                                                       QLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN 420
                                                                                                                                                                                                                                                                                                                                                  SOGDMODINGNNOSVTROKMOOLEOMLTALDOMRRSIVSELAGILSAMEYVQKTLTDEEL
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PEGL-IFWTKFCK-SLNEKSFPFWLWIEAILDLIKRHLLSLWNDGCILGFVSKEREKALL
                    YSGCQI "WAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAIL 598
                                                                                                                                                                                                                                                                QLKVKALFDK---DVTEKKGFRKFNILGTNTKVLNMEES-NGSLAAEFRHLQLKEQKVA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NR--EHPMAGLTPKOLEHEKLLIAEMCLKLKIKRGEVVGQLAEVLNMAEAVQSDLISEEL
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51.48;
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EMBL/GenBank/DDBJ
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Pred. No. 1
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1.4e-120;
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RESULT 10

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ID 013132

AC 013132;

DT 01-JUL-1997

DT 01-JUL-1997

DT 01-JUN-2001

DE STAT1-2.

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Best Local Similarity
Matches 379; Conser
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InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 754 AA; 87147 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Crantlata; Vertebrata; Euteleos
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson M.C., Mourich D.V., Leong J.C.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ EMBL, U60332; AAB0925.1; -. HSSP; P42224; 1BF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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QLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN
                                  PEWKKROQSSCIGRPPNACLDQLQNWFTAVAESLQQVRQQLKELQELEQKYTYDNDPIKQ
                                                                                                    ADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQ :||:|:::||:||:||:||:||:||:||:||:||
                                                                                                                                      NR--EHEINGLTPKQLEHEKLQIVEMCFKLKFKRVEVVGQLAEVLNMAEAVQSDLISEEL
                                                                                                                                                     AKSIETDRENTQTSMVL--EKQKLDNKVKDMKNKVQEADQNIKSLEYLQDERDFKENILK
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51.2%;
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Pred. No. 6.5e-120;
0; Mismatches 201;
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5.5e-120;
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBL_TaxiD: 7955;
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PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thesis (1998), University of Melbourne, EMBL; AJ005692: CAA06676.1; -.
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LKSQGDMQDLNG--NNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLT
                                                                                                                                  AATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKT
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                                                                        -AIAGMSESPTPNPTQDMIVEKNREMDARVKDIKNKVQDAEQTIKNLEDLQDEYDFKNKT
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SM: 2; SH2; 1.

; PS50001; SH2; 1.

E 744 AA; 86856
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
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STAT.
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                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
TRANSCRIPTION FACTOR STAT3 (FRAGMENT).
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Miyoshi K., Cui Y., Riedlinger G.,
Oka T., Dewar K., Hennighausen L.;
"Structure of the Mouse Stat 3/5 Lo
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
NON_TER
SEQUENCE
                                                                                                                                                                                       Genomics 0:0-0(2001).
EMBL; AF322857; AAG42495.1;
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  394 AA;
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  2BDEDFE716B50E70 CRC64;
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Q9QXJ2
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Matches 317; Conserv
                                                                                                                                                                                           InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00352; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 922 AA; 105385;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-B10.A; Farrar J.D., Smith J.D., Murphy T.L., Murphy K.M.; Farrar J.D., Smith J.D., Murphy T.L., Murphy K.M.; Sequence Divergence in the C-Termini of Murine an Controls Species Specific Stat4 Activation and Th1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9QXJ2 PRELIMINARY; PRT; 922 AA.
Q9QXJ2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAT2.
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF206162; AAF17096.1;
HSSP; P42224; 1BF5.
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Submitted (NOV-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MAQWEMLQNLDSLFLDQLHQVYSQSILPMDVRQHLATWIEDQNWREAALGSDDAKANMLY
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                                                                                                        Similarity
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                                                                                   31.9%; Score 1287; DB 11; 39.3%; Pred. No. 7.3e-79; ive 140; Mismatches 259;
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Sciurognathi; Muridae;
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SEQUENCE FROM N.A.

TISSUB=THYMUS;
MEDLINE=99449725; PubMed=10518610;
Park C., Lecomte M.-J., Schindler C.;
"Murine Stat2 is uncharacteristically di
Nucleic Acids Res. 27:4191-4199(1999).
EMBL; AF187231; AAF01441.1; -.
HSSP; P42224; 1BF5.
InterPro; IPR001980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
NCBI_TaxID-10090;
                                                                                                                                                                              Q9QZE4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYK--TLKSQGDMQDLNGNNQSYTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQ | :|| :| :| :: ;|:|: :: ;|:|: ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTAATAAQQGGQANHPTA--AVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSILDQLN-QWDHYSSDSNHFLLQHNLRKFSRDIQT-FPNGPTQLAEMIFNLLLEEQRIL
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                                                                                                                                                                                                                                                                                                             HKLIVI -----
                                                                                                                                                                                                                                                                                                                              TKFICVTPTTCSNTIDLPMSPRTLDSLMQ
                                                                                                                                                                                                                                                                                                                                                        LPLTEIIRHYQVLAEENIPENPLRFLYPRIPRDEAFGCYYQEKVNFEEQ---
                                                                                                                                                                                                                                                                                                                                                                      MSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEKLLGPGVNYSGCQITWAKFCK-ENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTLVDLLLPKLDEWKVQQQKSCIGAPPPELQLEQLEQWLTAGAKFLFHLRQLLKQLKEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTLTD---EELADWKRRPEIACIGG-PPNICLDRLENWITSLAESQLQTRQQIKKLEELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYTVFSLKKTSS----SDPHQS---QQQQLVQATANKVDRMRKEVLDISKGLVGRL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOAQRAQEVQPPPAPEAVVESQQLEIENRIQGLHVDIEFLVRSIRQLKDEQDVFSF
                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                             SNRQVDELQQ
                                                                                                                                                                                        nnotation update)
TRANSCRIPTION 2.
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                                                                      divergent
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                                                                                                                                                      Muridae;
                                                                                                                                                                   Euteleostomi;
                                                                                                                                                       Murinae;
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RESULT
Q9DG74
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AC Q0
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Best Local S
Matches 292
                   Q9DG74 PRELIMINARY;
Q9DG74;
Q9DG74;
Q1-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-JUN-2001 (TrEMBLrel. 17, L
SIGNAL TRANSDUCER AND ACTIVAT
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SMART; SM00252; SH2; 1.
PROSITE; PF550001; SH2; 1.
SEQUENCE 925 AA; 105742 MW;
   Oncorhynchus
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                                                                                                                                                                                                                                            HKLIVI - - - - - -
                                                                                                                                          TKFICVTPTTCSNTIDLPMSPRTLDSLMQ
                                                                                                                                                                         FISKEGERALLSTKPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQI.NN
                                                                                                                                                                                                                                                                                  QLSIAWASILWENMLSPNPKNQQFFCQAPKAPWSLLGPVI.SWQFSSYVGRGRDSEQI.GML
                                                                                                                                                                                                                                                                                              QMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQIJTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTLTD---EELADWKRRPEIACIGGP-PNICLDRLENWITSLAESQLQTKQ1KKLEEIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYK--TIKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLI.SAMEYVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTAATAAQQGGQANHPTA--AVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAQWEMLONLDSLFLDQLHQVYSQSILPMDVRQHLATWIEDQNWREAALGSDDAKANMLY
                                                                                                                                                               LPLTEI1 KHYQVLAEENIPENPLRFLYPRIPRDEAFGCYYQEKVNFEEQ
                                                                                                                                                                                                    FVSRNORERLLKKMLSGTFLLRFSETS-EGGITCSWVEHQDDDKVEIYSVQPYTKEVLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                               TTLVDLLLPKLDEWKVQQQKSC1GAPAPELQLEQLEQWLTAGAKFLFHLkQLI.KQLKEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYTVFSLKKTSS----SDPHQS---QQAQLVQATANKVDRMRKEVLDISKGLVGRL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292;
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   mykiss
   (Rainbow
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    16, Last sequence update)
    17, Last annotation update)
    ACTIVATOR OF TRANSCRIPTION 5.

                                                                                                                        -SNRQVDELQQ
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Pred. No. 1.1e-78;
40; Mismatches 262
   trout)
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  (Salmo
                                                                      784
                                                                      AA
  gairdneri)
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A Johnson M.C., Mourich D.V., Leong J.C.;

"Rainbow Trout STAT Genes: Evolutionary Duplication Leads to mand the Acquisition of Mammalian Specific Function.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF147499; AAG14946.1; -

R Interpro; IPR001980; SH2.

R Interpro; IPR001217; STAT.

R Pfam; PF01017; SH2; 1.

R Pfam; PF01017; STAT; 1.

R SMART; SM00252; STAT; 1.

R SMART; SM00252; STA; 1.

R PROSITE; PS50001; SH2; 1.

R SEQUENCE 784 AA; 89780 MW; 1C16D6CF7C83AF7C CRC64;
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Best Local Similarity
Matches 248; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. NCBI_TaxID-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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YCRPESQEHPEADPGSAA--PYLKTKFICVTPTTCSNTIDLPMSPRTLDSLMQFGNNGEG
                                                      VMELTKKHLKPHWNDGAILGEVNKQQAQDMLMSKPNGTFLLRESD-SEIGGITIAWVAEN
                                                                                                                          IIDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKD
                                                                                                                                                                                                          S--TTKRGLSIEQLTTLAEKLLGPGV----NYSGCQITWAKFCKENMAGKGFSFWVWLDN
                                                                                                                                                                                                                                                                                                                 YHQA-TGTLSANFRNMSLK--RIKRSDRRGAES---VTEEKFTILFESQFSVGGNELVFQ
                                                                                                                                                                                                                                                                                                                                                 MEESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQG--LKID
                                                                                                                                                                                                                                                                                                                                                                                                            QFTTKVRLLVKFPELNYQL---KIKVCIDKDSGDVAALRGSRKFN-----ILGTNTKVMN 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPIVIKTGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y-KTLKSQGDMQDL-----NGNNQSVTRQKMQQLEQMLT----ALDQMRRSIVSELAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REASNSSSPVGGMMDS-----MSQKYQQINQAFEELRLLTQDTENDLRKLQHNQEYFIIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FHNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAVWIQAQQLQGDALHQMQSLYGQHFPIEVRHYLSQWLEGQLWDVIDLENPQEEFKAKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYA----ASKESHATLV
                                PNKPGERMVWNLMPYTTKDFSIRSLAD-----RISDLNHLL-----FLYPDRPKDEVFSK
                                                                                                                                                                         {\tt AEVQSNRGLSEENLVFLAQKAFSSSSINPDDYRGMTMTWSQFNRESLPGRNFTFWQWFDG}
                                                                                                                                                                                                                                             VKTLSLPVVVIVHGSQDNNATATVLWDNAFA-EPGRVPFIV-PDKVLWPQLCEALNMKYK
                                                                                                                                                                                                                                                                            LETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFS
                                                                                                                                                                                                                                                                                                                                                                                    KFAATVRLLVG-GKLNVHMNPPQVKATIISEQQAKALLKNENTRNDSSGEILNNNC-VME
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEHLRQQLPIPG-PIEELLNDLNSTITDIISALVTSTFIIEKQP-----PQVLKTQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.7%; Score 873; DB 30.4%; Pred. No. 6.6e tive 151; Mismatches
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No. 6.6e-51;
smatches 314; Indels 104;
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                  744
                                      686
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| YYTP---
ASPVVSHPPNYGIYQPMSDSILDADGDFDLDDTMDVA 764
                  AEPSAG----
                  -GQFESI.T-----
                                    -PLSKAVDGYVKPQIKQVVPEFTTTNPDPAANPTYMD---
                  FDMULTSECA 766
                                      품...
                                      7:27
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Search completed: Job time: 226 sec March 19, 2002, 15:25:44

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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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RAST_LOROME
RAZC_YEAST
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Best Local Similarity 99.5
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InterPro: IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00255; SH2; 1.
PROSITE; FS50001; SH2; 1.
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X-RAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716. MEDLINE=9834373; PubMed=9671298; Becker S., Groner B., Mueller C.W.; "Three-dimensional structure of the Stat3beta homo
                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 394:145-151(1998) -i- FUNCTION: TRANSCRIPT
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                  Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC;
                    ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIDNEY STAT3B IS ALSO DETECTED IN THE LIVER, ALTHOUGH IN A MUCH LESS ABUNDANT MANNER.

PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-ALPHA AND OSM. SERINE PHOSPHORYLATION IS IMPORTANT FOR THE FORMATION OF STABLE DNA-BINDING STAT3 HOMODIMERS AND MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY). SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS. SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE INTERLEUKIN-6 (IL-6)-RESPONSIVE ELEMENTS IDENTIFIED IN THE PROMOTERS OF VARROUS ACUTE-PHASE PROTEIN GENES. STAT18 INTERACTS WITH THE N-TERMINAL PART OF C-JUN TO ACTIVATE SUCH PROMOTERS IN A COOPERATIVE WAY.

PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.

SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAMILY MEMBER (AT LEAST STAT1) (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN RESPONSE TO PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: STAT3A IS SEEN IN THE LIVER, SPLEEN, A
KIDNEY. STAT3B IS ALSO DETECTED IN THE LIVER, ALTHOUGH IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: 2 ISOFORMS; STAT3A (SHOWN HERE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; L29278; AAA37254.1;
; U06922; AAA19452.1;
; U08378; AAA56668.1;
; U30709; AAC52612.1;
MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:103038; Stat3
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727
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                                          ; Score 4010; D
; Pred. No. 8.4e
3; Mismatches
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MISSING (IN
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ACTIVATION.
E -> K (IN
S -> T (IN
M -> I (IN
                                                                                                                                                                                                                                                                                                    splicing;
SH2.
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TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT

TCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                                                                                                                                                                                                                                                      PHOSPHORYLATION
                                                                                                                -> K (IN REF. 2).
-> T (IN REF. 2 AND 4).
-> I (IN REF. 1).
6C00626711C8012D CRC64;
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                                                        DB 1;
3.4e-244;
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PRT; 770 AA. 11; 77-1996 (Rel. 34, Created) 77-1996 (Rel. 34, Last sequence update) 77-1997 (Rel. 35, Last annotation update) V-1997 (Rel. 35, Last annotation update) NL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3. IS NOTVEGICUS (Rat). Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Yilia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. TaxID=10116; NRCE FROM N.A. FELLVer; NE=96102059; PubMed=8530402; RFGET J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F., H.; Scription factors Stat3 and Stat5b are present in rat liver il late in an acute phase response and bind interleukin-6	DATNILVSPLYYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720	ITWAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALMNEGY:	IKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN 42 IKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN 42 ANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVISNICQMPNAWASILWY 48 ANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVISNICQMPNAWASILWY 48 ANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVISNICQMPNAWASILWY 48 TNNPKNVNFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYS 54 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	DWKRRPEIACIGGPPNICLDRLENWITSLAESQLOTROOIKKLEELOOKVSYKGI	MAQWNOLQQLDTRYLEQLHQLYSDSFPMELROFLAPWIESQDWAYAA;KESHATLVFHNL 60 LGEIDQOYSRFIQESNVLYQHNLRRIKQFLQSRYLEKPMEIAKIVARGLWEESKLIQTAA 120 [1] 1 1 1 1 1 1 1 1 1

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SEQUENCE
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Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Transcription regulation; DNA-binding;
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InterPro; IPR001217;
Pfam; PF00017; SH2; 1
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HSSP; P42224;
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- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO (IL-6)-RESPONSIVE ELEMENTS IDENTIFIED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.
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SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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                  QLKIKYCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGN
                                                                         HRPMLEERIVELERNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNY
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Pred. No. 1.3e
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P40763;
01-FEB-1995
01-FEB-1995
01-NOV-1997
                                                                                                                                                                                    Science
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   -!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE INTERLE (IL-6)-KESPONSIVE ELEMENTS IDENTIFIED IN THE PROMOTERS (ACUTE-PHASE PROFEIN GENES).
-!- PATHAY: INVOLVED IN THE GP130-MEDIATE) SIGNALING PATHAY.
-!- SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELAMEMBER (AT LEAST STAT1).
-!- SUBCELLILAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCRESPONSE TO PHOSPHORYLATION.
-!- TISSUE SPECIFICITY: HEART, BRAIN, PLACENTA, LUNG, LIVER, MUSCLE, KIDNEY, AND PANCREAS.
-!- PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-1], LIF, CSF-1, EGF, PDGF, IFN-ALPHA AND OSM. SERINE PHOSPHG IS IMPORTANT FOR THE FORMATION OF STABLE DNA-BINDING STAHMONOLIMERS AND MAXIMAL TRANSCRIPTIONAL ACTIVITY:
-!- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                               PHOSPHORY ON SERINE.
MEDLINE-W 13; PubMed-7701321;
Zhang X., ...mis J., Li H.-C., Sc
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01-FEB-1995 (Rel. 31,
01-NOV-1997 (Rel. 35,
SIGNAL TRANSDICER AND
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Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
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HSSP; P42224; 1BF5.
TRANSFAC; T01493; -.
MIM; 102582; -.
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Cell 82:2
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P42224;
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J. Biol. Chem. 270:20775-20780(1995).
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MEDLINE=98292180; PubMed=96
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FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (ISRE) AND TO THE GAS ELEMENT. THIS MULTIPROTE. TRANSCRIPTION FACTOR IS TERMED ISGF3.

TRANSCRIPTION FACTOR IS TERMED ISGF3.

PATHWAY: IFN-SIGNALLING PATHWAY:
SUBUNIT: IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STATI-SUBUNIT: IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STATI-ALPHA, STATI-BETA, STATI) OF ISGF3, BECOME PHOSPHORYLATED ON TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX TOGETHER WITH ISGF3 GAMMA (P48), A DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT. IN RESPONSE TO IFN GAMMA, STATI FORMS HOMODIMERS, THAT ALSO
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etazoa; Chordata;
theria; Primates;
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Thierfelder W., Witthuhn
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ISGF-3 COMPONENTS P91/P84).
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Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSLOCATE INTO THE NUCLEUS TO ACTIVATE IFN GAMMA-RESPONSIVE GENES. INTERACTS WITH NMI.
SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA/P91 (SHOWN HERE) AND
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Pred. No. 5
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S->A: DECREASED TRANSCRIPTIONAL
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          RA Zhong Z., Wen Z., Darnell J.E. Jr.;

RA Zhong Z., Wen Z., Darnell J.E. Jr.;

RT "Stat3 and Stat4: members of the family of signal transducers and RT activators of transcription.";

RI Proc. Natl. Acad. Sci. U.S.A. 91:4806-4810(1994).

CC -1- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (ISRE) AND TO THE GAS ELEMENT. THIS MULTIPROTEIN C.

C. TRANSCRIPTION FACTOR IS TERMED ISGF3.

C. -1- SUBUNIT: IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STAT1-ALPHA, STAT1-BETA, STAT2) OF ISGF3.

C. TRANSCRIPTION FACTOR THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX TYROSINE WITH ISGF3 GAMMA (P48), A DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT. IN RESPONSE TO IFN GAMMA, STAT1 FORMS HOMODIMERS, THAT ALSO TRANSLOCATE INTO THE NUCLEUS TO ACTIVATE IFN GAMMA-RESPONSIVE.

GENES. INTERACTS WITH NMI (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN RESPONSE TO PHOSPHORYLATION.

-1- INDUCTION: BY IFN AND EGF.

-1- PTM: TYROSINE PHOSDHORY.----
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P42225;
01-NOV-1995
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Eukaryota; Metazoa;
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20-AUG-2001
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Metazoa; Chordata; C
Metazoa; Rodentia; S
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
SDU:ER AND ACTIVATOR OF TRANSCRIPTION 1.
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  SERINE
PHOSPHORYLATION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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IFN-ALPHA,
FOR MAXIMAI
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Query Match
Best Local 9
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InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:103063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
WYNMLYTEPRNLSFFLNPPCAWWSQLSEVLSWQFSSVTKRGLNADQLSMLGEKLLGPNAG
                                                                                                                                                           GNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASIL
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                                                                                                  WYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVN
                                                                                                                                    -NAGNRTNEGPLIVTEELHSLSFETQLCQPGLVIDLETTSLPVVVISNVSQLPSGWASIL
                                                                                                                                                                                                                  NLLTKVKCHFDKDVNEKNTVKGFRKFNILGTHTKVMNMEESTNGSLAAELRHLQLKEQK-
                                                                                                                                                                                                                                    NYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNNEESNNGSLSAEFKHLTLREQRC
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51.0%;
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Pred. No. 6
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249D919952BE65F1 CRC64;
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Conservative

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Query Match
Best Local Similarity
Matches 357; Conserv
                                                                                                                                                                                                                                                                                                          InterPro; IPR001217; STAT
Pfam; PF00017; SH2; 1.
Pfam; PF0101017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
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30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
SIGNAL TRANSDUCER A
                                                                                                                                  MOD_RES
SEQUENCE
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CARRIES OUT A DUAL FUNCTION: SIGNAL TRANSDUCTION
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Q14765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                       Phosphorylation;
DOMAIN 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L78440; AAB05605.1; MIM; 600558; -.
                                                                                                                                                                                                                                                                                    Transcription regulation; DNA-binding; Nuclear protein;
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Eukaryota; Metazoa;
                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000980;
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*The STAT amino-terminal domain mediates cooperative DNA binding
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†heria: Primates; Catarrhini; Hominidae
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                                                                                                                               PHOSPHORYLATION (BY JAKS) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARIT 11643803A9AF4FFA CRC64;
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MEDLINE=94255416; PubMed=7545930; Zhong Z., Wen Z., Darnell J.E. Jr "Stat3 and Stat4: members of the
                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                         TISSUE=Thymus;
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                                                                                               Chordata;
Rodentia;
 the family
                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local
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InterPro; TPR0011217; STAT.
Pfam; PF00; 7 - 442; 1.
Pfam; PF01 - FAT; 1.
SMART; SW ...; SH2; 1.
                                                                                                                                                                        MOD_RES
CONFLICT
CONFLICT
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MEDLINE-9427703B; PubMed-8007943;
Yamamoto K. Quelle F.W. Thierfelder W.E.,
Gilbert D.J., Jenkins N.A., Copeland N.G., S
                                                                                                                                                                                                                                          Transcription regulation; DN
Phosphorylation; SH2 domain;
DOMAIN 570 665
MOD_RES 694 694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION OF TRANSCRIPTION.
-!- SUBUNIT: FORMS A HOMODIMER OR A HETEKODIMER MEMBER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98128033; PubMed=9461439;
Vinkemeier U., Moarefi I., Darnel
"Structure of the amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U06923; AAA19453.1; EMBL; U09351; AAA19692.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: NUCLEAR; RESPONSE TO PHOSPHORYLATION.
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                                                                                                                      Local Similarity
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                                                                MAQWNOLCOLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL
 LIQLDEOLGRVSKEKNLLLIHNLKRIRKVLQGKFHGNPMHVAVVISNCLREERRIL-AAA
                                                   MSQWNQVQQLEIKFLEQVDQFYDDNFPMEIRHLLAQWIETQDWEVASNNETMATILLQNL
               LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLLQTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel gamma interferon activation site-binding in early myeloid differentiation."; . Bi.l. 14:4342-4349(1994).
                                                                                                                                                                                                                                                                                                                                                                                         201576;
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                                                                                                         Conservative 149;
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A -> P (IN REF. 2)
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                                                                                                                   Score 1780.5;
Pred. No. 3.8
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                                                   Proc. Natl. Acad. Sci.
                                                                                                       MEDLINE=92366558;
Fu X.~Y., Schindle
"The proteins of
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ALTERNATIVE SPLICING
                                                                                                                                                                                 SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                  R., Qureshi S., Zhong Z., Wen Z., Darre genomic structure of the STAT genes: noident sittes in Stat1 and Stat2."; leic Acids Res. 23:459-463(1995).
                                              .-Y., Schindler C., Improta T., Aebersold R., Darnell J.E. Jr.; proteins of ISGF-3, the interferon alpha-induced transcriptional vator, define a gene family involved in signal transduction."; Natl. Acad. Sci. U.S.A. 89:7840-7843(1992).
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                                                                                                                                                        PubMed=1502204;
                                                                                                                                                                                    AND PARTIAL SEQUENCE
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Best Local S
Matches 298
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C -I- SUBUNIT: IN RESPONSE TO IFN ALDHA/BETA, THREE SUBUNITS (STAT1-ALDHA, STAT1-BETA, STAT2) OF ISGF3, HECOME PHOSPHORYLATED ON TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX TOGETHER MITH ISGF3 GAMMA (P48), A DAN-BINDING PROTEIN THAT SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT.

C -I- SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN RESPONSE TO PHOSPHORYLATION.

C -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

C -I- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.

C -I- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR000980; SH2
InterPro: IPR001217; STAY
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                            VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U18671; AAA98760.1; EMBL; M97934; -; NOT_ANNOTED_CDS. EMBL; S81491; AAB36226.1; EMBL; S81491; AAB36227.1; ALT_SEQ. HSSP; P42224; 1BF5.
                                                                                                                                                                                                                                                                                                                                                                                                                      MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Stat2 is a transcriptional activator that requires sequence-specific contacts provided by stat1 and p48 for stable interaction with DNA."; J. Biol. Chem. 272:4600-4605(1997).
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                                                                                                                                                                                                                                                                                                   Phosphorylation; SH2 domain;
DOMAIN 572 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bluyssen H.A., Levy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97172544; PubMed-9020188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                           Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50001; SH2; 1.
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                 117
                                        61
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                                                                                                                       <del>ب</del>
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
SWISS-PROT entry is copyright. It is produced through a comethe swiss Institute of Bioinformatics and the EMBL
                                                    600556
                                     FHFLDQLNYECGRCSQDPESLLLQHNLRKFCRDIQP-FSQDPTQLAEMIFNLLLEEKRIL
                                                                                                                                                          Similarity
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851
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97916
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690
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Pred.
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                                                                                                                                                                                                                      PAIPTASPFCLAPLLPLCLPLASLALN ISOFORM). MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY JAKS) (BY SIMILARITY).

DKVLIYSVQPYTKEVLQSLPLTEIIRHYQLLT ->
                                                                                                                                                                                                         E4C74674CB7A3215 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splicing form
                                                                                                                                            Mismatches
                                                                                                                                                          1293;
No. 1
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                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
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V SHORT
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STRAIN=CD-1;
Paulson M.S., Mui A., Levy D.E.
"Molecular cloning and characte
"Molecular cloning and characte
Submitted (AUG-1998) to the EMB
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20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
Sugiyama T., Nishio Y., Kishimoto T., Akira S.;
"Identification of alternative splicing form of Stat2.";
FEBS Lett. 381:191-194(1996).
-!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (IREE) AND TO THE GAS ELEMENT. THIS MULTIPROTEI TRANSCRIPTION FACTOR IS TERMED ISGF3.
-!- SUBUNIT: IN RESPONSE TO IFN ALPHA/PPT"
                                                                                                                                                                                                                                                                                                                                                                                                     _MOUSE
STA2_MOUSE
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                             SIGNAL TRANSDUCER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHYQLLTEENIPENPLRFLYPRIPRDEAFGCYYQEKVNLQERRK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGYKIMDATNILVSPLYYLYPDIPKEEAFGKYCRPE--SQEHPEADPGSAAPYLKTKFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCRTEDPLLSWADFTKRESPPGK-LPFWTWLDKILELVHDHLKDLWNDGRIMGFVSRSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVNYSGCQITWAKFCK-ENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERE 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEGNESLTVEVSIDRNP----PQLQGFRKFNILTSNQKTLTPEKGQSQGLIWDFGYLTLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPLTKGVDLRNAQVTELLQRLLHRAFVVETQPCMPQTPHRPLILKTGSKFTVRTRLLVRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-PKLEEWKAQQQKACIRAPIDHGLEQLETWFTAGAKLLFHLRQLLKELKGLSCLVSYQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVLWFNLLSPNLQNQQFFSNPPKAPWSLLGPALSWQFSSYVGRGLNSDQLSMLRNKLFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRSGGSGKGSNKGPLGVTEELHIISFTVKYTYQGLKQELKTDTLPVVIISNMNQLSIAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YK-IQAKGKTPSLDPH--QTKEQKI--LQETLNELDKRRKEVLDASKALLGRLTTLIELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQAQRAQLEQGE---PVLETPVESQQHEIESRILDLRAMMEKLVKSISQLKDQQDVFCFR
                                                                                                                                                                                                                                                                                                           STANDARD,
19; Q64250; Q64188;
19; Q64250; Q64188;
(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                  (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SNRQVDELQQ-----
                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                  Levy D.E.;
d characterization of murine Stat2.";
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - PLELKPEPELESLELELGLVPE
                                                                                                                                                                                                                                                                     Muridae;
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                                                 MULTIPROTEIN
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Matches 292
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                              MAQWNQLQQLDTRYLKQLHQLYSDTF-PMELRQFLAPWIESQDWAYAA--SKESHATLVF 57
    QKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTK
                                                                                                                                                                                                                                HNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLIQ 117
                                                                                                                                                                                                                                                               MAQWEMLQNLDSPFLDQLHQVYSQSFLPMDFRQHLASWIEDQNWREAALESDDAKANMLY
                              TLVDLLLPKLDEWKVQQQKSCIGAPPPVKSAAEQLEQWLTAGAKFLFHLRQLLKQLKEM-
                                                               TLTD---
                                                                                           TYTY
                                                                                                                  YKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTA--LDQMRRSIVSELAGLLSAMEYVQK
                                                                                                                                               --- IQAQRAQEVQPPPAPEAVVESQQLEIENRIQGLHVDIEFLVRSIRQLKDEQDVFSFR 175
                                                                                                                                                                          TAATAAQQGGQANHPTA--AVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFN 175
                                                                                                                                                                                                        FSILDQLNQWDHYSSDPKSLLLQHNLRKFSRDIQP-FPNGPSQLAEMIFNLLLEEQRIL- 118
                                                                                                                                                                                                                                                                                                                                      Similarity
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EELADWKRRPEIACIGGPPNI -- CLDRLENWITSLAESQLQTRQQIKKLEELQ

-SLKKTSSSDPHQSQQAHVVQATANKVDRMRKEVLDISKGLVGRL----T

233 224

Conservative

31.6%; 133;

Score 1271.5; D Pred. No. 4e-72; 3; Mismatches 2

DB 1; 265;

923; 63;

Indels Length

Gaps

18

60

δÃ В Qy DЬ Qy DЬ Qγ DЪ Q 망 Qy Ъ Qy ф ρy В δÃ В 20 В

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InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF088862; AAD38329.1; -
EMBL; S81342; AAB36228.2; -
EMBL; S81342; AAB36231.1; -
EMBL; S81342; AAB36230.1; ALT
HSSP; P42224; 1BF5.
MGD; MGI:103039; Stat2.
                                                                                                                                                                                                     Phosphorylation;
DOMAIN 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                     Transcription regulation; DN. Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for comitties requires a license arrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX TOGETHER WITH ISGF3 GAMMA (F48), A DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN RESPONSE TO PHOSPHORYLATION (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B/C; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: FOUND THE THESTIS.

TYROSINE PHOSPHORYLATED IN RESPONSE TO IFN-ALPHA (BY FYM. TYROSINE PHOSPHORYLATED IN RESPONSE TO IFN-ALPHA (BY FYM. TYROSINE PHOSPHORYLATED IN RESPONSE TO IFN-ALPHA (BY
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620
923 AA;
                                              1.44
6
                                                                                                                                                                           689
                                            923
596
105416 MW;
                                                                                                                                                                                                                                               DNA-binding; Nuclear protein;
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                                            SARHPIRTLPP (IN SHORT ISOFORM)
MISSING (IN SHORT ISOFORM)
T -> A (IN REF 2)
                                                                                                                                                 SIMILARITY)
                                                                                                                                                                      PHOSPHORYLATION (BY JAKS)
                                                                                                                                                                                                                        Alternative
                                                                                                                  HKVEIYSVQPYTKEVIQSLPLTEI -> GQHPPPYHSCSLL
                       -> A (IN REF. 2).
-> D (IN REF. 2).
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D50BB54C535B0774 CRC64;
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the European constitutions as consumed by and to consume by non-profit institutions as consumed by and this statement is not removed. Usage by and to entitles requires a license agreement (See http://www.isb-sib.ch/announce/and an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STA2_PIG
002799;
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the Euro
                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                           Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      689
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                                                                                                                                                RESPONSE TO PHOSPHORYLATION (BY PTM: TYROSINE PHOSPHORYLATED IN SIMILARITY).

SIMILARITY: BELONGS TO THE STAT SIMILARITY: CONTAINS 1 SH2 DOMAI
                                                                                                                                                                                                                                                TY, MIKAWA S., KODAYAShi E., WAGA Y., MINEZAWA M.;

WILLIAM S., KODAYAShi E., WAGA Y., MINEZAWA M.;

WILLIAM S., KODAYAShi E., WAGA Y., MINEZAWA M.;

WILLIAM S., KODAYASHI S., WAGA Y., MINEZAWA M.;

WILLIAM S., WALTED ALL STATED ALL STATE STIMULATED TO THE TRANSCRIPTION FACTOR IS TERMED ISGF3 (BY SIMILARITY).

SUBUNIT: IN RESPONSE TO IFN ALPHA/BETA, THREE SUBUNITS (STAT1-ALPHA, STAT2) OF ISGF3, BECOME PHOSPHORYLATED ON TYROSINE, MIGRATE INTO THE NUCLEUS, AND ASSEMBLE INTO A COMPLEX SPECIFICALLY BINDS TO THE IFN-STIMULATED RESPONSE ELEMENT (BY STEEL STATE).
                                                                         by non-profit institutions as long
                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE RESPONSE TO PHOSPHORYLATION (BY SIMILARITY).
PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IFN-ALPHJ
                                                                                                                                                                                                                                        SPECIFICALLY BINDS SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRP----ESQEHPEADPGSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFLTLVEQRAVGAGKGNNKGPLAVTEELHVISFVVEYTYQGLKMKLQTDTLPVVIISNMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCLRYQGDMFAKGVDLRNAQVMELLQRLLQRSFVVETQPCMPQTLHRPLILKTGNKFTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -YLKHKLIVI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPLTEIIRHYQVLAEENIPENPLRFLYPRIPRDEAFGCYYQEKVNLEEQEE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTKLFGKSCKMEDALLSWVDFCKRESPPGK-IPFWTWLDKILELVHDHLKDLWKDGRIMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEKLLGPGVNYSGCQITWAKFCK-ENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRLLVRLQEGSESLKAEVSVDRNSD----LPGFRKFNILTSNQKTLTPEKGQRQGLIWDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYLKTKFICVTPTTCSNTIDLPMSPRTLDSLMQ 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVSRNQERRLLKKMLSGTFLLRFSETS-EGGITCSWVEHQDDHKVEIYSVQPYTKLVLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38, Created)
38, Last sequences and ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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Last annotation update)
ACTIVATOR OF TRANSCRIPTION
                                                                                                                                                   THE STAT FAMILY OF SH2 DOMAIN.
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Query Match
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Matches 292
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Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PR0SITE; PS50001; SH2; 1.
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DOMAIN 572 667 SH2.
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InterPro; IPR001217; STAT
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                                                                                 MGYKIMDATNILVSPLVYLXPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFJCVT 714
                                                                                                                                                                                                                     GVNYSGCQITWAKFCK-ENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERE
                                                                                                                                                                                                                                                                                                                             QRCGNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRQVDELQQPPELKLEPDLESLELDLGLAP - -
                                                                                                                            RRLLKKTISGTFLLRESE-TLEGGITCSWVEHQDDDKVLIVSLQPFTKEVLQSLPLTKII 645
                                                                                                                                                  RAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEII 654
                                                                                                                                                                                               NSSTEGLSLSWVDFIKRESPPGK-LPFWTWLDKILDLVHDHLKDLWKDGHIMGFVSRSEE
                                                                                                                                                                                                                                                               SILWFNLLSSDPQNQQFFSSPPKAPWNLLGPALSWQFSSHVGQGLNSDQLGMLRDKLFGQ
                                                                                                                                                                                                                                                                                              SILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGP
                                                                                                                                                                                                                                                                                                                                                                                                                             PELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGS1.SAEFKHLTLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-PKLEEWKVQQQKACIGAPMDGELEQLEKWFTAEAKLLFHLRQLLKELKGLSSVVKYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKG
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                                                              SQYQLLTEENIPENPLRFLYPRIPRDEAFGCY----NQE--KANLQERKKYLKHKLIVVS 699
                                                                                                                                                                                                                                                                                                                                                                                                QEGNESITAEVSTORNP----PKSQGFRKFNILTSNRKTLTPEKGQSQGLIWDFGYLTLME
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLLFKGVDLLKAQVTELLQRLLHRAFIVETQPCMPQTPHRPLILKTGSKFTVRTRLLVRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQAQRAQL---EQQEPALEAPGENQQHEIESRILELRAMMEKLVKSISQLKDQQDIFCFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTAATAAQQGGQANHPTAAVVTEKQQ-MLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFN 175
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                               PTTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESL
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Pred. No. 9.9
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2F8CC95569FB5B20 CRC64;
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GPEPGVGLDLEPL
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RESULT 1
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Best Loc
Matches
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InterPro: IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                            VARIANT
VARIANT
VARIANT
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palin M.F., Beaudry D., Roberge C., Farmer C.;
Submitted (wAR-1999) to the EMBL/GenBank/DDBJ databases.
-I-FUNCTION: CARRIES OUT A DUAL FUNCTION: SIGNAL TRANSDUCTION
-ACTIVATION OF TRANSCRIPTION. BINDS TO THE GAS ELEMENT AND
-ACTIVATES PRL-INDUCED TRANSCRIPTION (BY SIMILARITY).
-I-SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED
MEMBER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  Phosphorylation;
DOMAIN 589
                                                                                                                                                                                                                                                                                                                                                              EMBL; AF135122; AAD46163.1; HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823;
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20-AUG-2001
                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                              Transcription regulation; DN Phosphorylation; SH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2001
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 13
                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THROMBOPOIETIN. TYROSINE PHOSPHORYLATION IS REQUIRED FOR DNA-BINDING ACTIVITY AND DIMERIZATION. SERINE PHOSPHORYLATION IS ALS REQUIRED FOR MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY). SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS. SIMILARITY: CONTAINS I SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO RESPONSE TO PHOSPHORYLATION (BY SIMILARITY). PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2, 15, GM-CSF, GROWTH HORMONE, PROLACTIN, ERYTHROPOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                 European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scrofa (Pig)
LENLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQNTYDRCPMELVRCIRHILYNEQRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collable of the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                             FHNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLL
                                               MAGWIQAQQLQGDALRQMQVLYGQHFPIEVRHYLAQWIESQPWDAIDVDNPQDRAQATQL
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240; Conser
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711
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711
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Cetartiodactyla; Suina;
                                                                                                             21.5%;
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Last annotation update)
ACTIVATOR OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                 138;
                                                                                                                                                                                                                                                                       DNA-binding;
                                                                                                                                                              ž
                                                                                              Score 867; DB
Pred. No. 7.1e
38; Mismatches
                                                                                                                                                                       SIMILARITY).
C -> R.
F -> S.
F -> L.
T -> I.
                                                                                                                                                                                                                                     PHOSPHORYLATION
                                                                                                                                                                                                                                                              Polymorphism.
                                                                                                                                                              310C123A8B624FF4
                                                                                                            867;
No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                        Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata;
ina; Suidae;
                                                                                                            DB 1;
.le-47;
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                                                                                                 303;
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                                                                                                                      Length
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Sus.
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                                                                                             Gaps
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RESULT 12
ST5B_MOUSE
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                                                                                                                                                                                                                                                                                                                    ST5B_MOUSE STANDARD;
P42232; Q60804;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
20-AUG-2001 (Rel. 40, Last ann
                                                                                                       Mui A.L.-F., Wakao H., O'Farrell A.-M., Harada N., Miyajima A "Interleukin-3, granulocyte-macrophage colony stimulating fac interleukin-5 transduce signals through two STATS homologs."; EMBO J. 14:1166-1175(1995).
 Liu X., Robinson G.W., Gouilleux F., Grone
"Cloning and expression of Stat5 and an ac
involved in prolactin signal transduction
                                               MEDLINE=96004632;
                                                                 STRAIN-C57BL/6
                                                                             SEQUENCE FROM
                                                                                                                                                                   STRAIN-C57BL/6 X A/J; TISSUE-Liver; MEDLINE-95237198; PubMed-7720707;
                                                                                                                                                                                                                                                                                       STAT5B
                                                                                                                                                                                                                                                                                                         SIGNAL TRANSDUCER
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              Mammalia;
                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PESQEHPEADPGSAAP----YLKTKFICVTPTTCSNTID 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPDRNLWNLKPFTTRDFSIRSLAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTLSL/PVVV1VHGSQDHNATATVLWDNAFA-EPGRVP-FAVPDKVLWPQLCEAL/NMKFKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HQA-TGTLSAHFRNMSLKRIK-----RADRRGAESVTEEKFTVLFESQFSVGSNELVFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETE--VYHQGLKIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAATVRLLVG-GKLNVHMNPPQVKATIISEQQAKSLLKNESTRNECSGEIL-NNCCVMEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTTKVRLLVKFPELNYQL---KIKVCIDKDSGDVAALKGSRKFN----ILGTNTKVMNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHLCQQLPIPG-PVEEMLAEVNATITDIISALVTSTFIIEKQP-----PQVLKTQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQLLRKQQT11LDDEL1QWKRRQQLAGNGGPPEGSLDVLQSWCEKLAE11WQNRQQ1RRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QESLRIQAQFAQLAQLNPQECLSRETALQQKQVTLEAWLQREAQTLQQYRVELAEKHQKT
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                                                                                                                                                                                                                                            Eutheria;
                                                                                                                                                                                                                                                         Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PVLAPASAAKAVDGYVKPQIKQVVPEFVSASSD
                                                                                                                                                                                                                                                                         (Mouse)
                                                                             N.A.
                                                                                                                                                                                                                                                                                                         AND
                                               PubMed=7568026;
                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
ACTIVATOR OF TRANSCRIPTION
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                                                                                                                                                                                                                                         Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLGD-----LSYL1YVFPDRPKDEVFSKYYT
Groner B., Hennighausen L.;
an additional homologue (Stat5b)
ction in mouse mammary tissue.";
                                                                                                                                                                                                                                                                                                                                                                                786
                                                                                                                                                                                                                                                         Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                ⋛
                                                                                                                                                                                                                                            Muridae;
                                                                                                                                                                                                                                                                                                       5B
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                                                                                                                                                                                                                                            Murinae;
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Query Match
Best Local S
Matches 247
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EMBL; U21110; AAC52282.1; -
HSSP; P42224; 1BF5.
TRANSFAC; T00944; -
MGD; 103035; Stat5b.
InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTOC. Natl. Acad. Sci. U.S.A. 92:8831-8835(1995).

-!- FUNCTION: CARRIES OUT A DUAL FUNCTION: SIGNAL TRANSDUCTION AND ACTIVATION OF TRANSCRIPTION. BINDS TO THE GAS ELEMENT AND ACTIVATES PAIL-INDUCED TRANSCRIPTION.

-!- SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAMILY MEMBER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUCLEUS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00017; SH2; 1.
Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
Transcription regulation; DNA-binding;
Phosphorylation; SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation;
DOMAIN 589
MOD_RES 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
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    297
                                           285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: DETECTED BOTH IN VIRGIN MOUSE AND A MANMARY GLAND INVOLUTION. THE LEVEL OF STATEA INCREASES DURING PREGNANCY, BUT DECREASES DURING LACTATION. PTM: TYROSINE PHOSEPHORYLATED.
SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESPONSE TO PHOSPHORYLATION.
TISSUE SPECIFICITY: IN THE VIRGIN, FOUN
PARTICULARLY ABUNDANT IN MUSCLE TISSUE
FEMALES, AND OF MALES.
                                                                                                                                                                                                                                                                           QTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNY
                                                                                                                                                                                                                                                                                                                     LEGLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQSTYDRCPMELVRCIRHILYNEQRLV
                                                                                                                                                                                                                                                                                                                                            MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYA----ASKESHATLV
EHLCQQLPIPG-PVEEMLAEVNATITDIISALVTSTFIIEKQP
                                     EELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQ
                                                                                                                   LSAMEYVQKTLTDEELADWKRRPE1ACIGGPPNICLDRLENWITSLAESQLQTRQQIKKL
                                                                                                                                                             QESTRIGAQEAQTGQTNbdcermsretalqqkqvstetwtqreaqttqqyrvetaekhqkt
                                                                                                                                                                                                    -KTLKSQGDMQDLNGNN-----
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                                                                                                                                                                                                                                                                                                                                                                                                     MAMWIQAQQLQGDALHQMQALYGQHFPIEVRHYLSQWIESQAWDSIDLDNPQENIKATQL
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786 /
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699
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Pred. No. 8.6e
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY JAKS)
SIMILARITY).
E -> G (IN REF. 2).
; A8FE76405E41B2EF CRC64;
                                                                                                                                                                                                -QSVTRQKMQQLEQML----TALDQMRRSIVSELAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH2
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3.6e-47;
hes 317;
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AND LACTATING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ST5B_RAT
P52632;
                                                                                                    SEQUENCE FROM N.A.

STRAIN-NOBLE; TISSUE-Lymph node;
STRAIN-NOBLE; TISSUE-Lymph node;
Luo G., Yu-Lee L.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

-i- FURCTION: CARRIES OUT A DUAL FUNCTION: SIGNAL TRANSDUCTION
-CONTROL OF TRANSCRIPTION. BINDS TO THE GAS ELEMENT AND
ACTIVATION OF TRANSCRIPTION. BINDS TO THE GAS ELEMENT AND
ACTIVATES PRL-INDUCED TRANSCRIPTION (BY SIMILARITY).

-i- SUBJUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPT
STAT5B.
                                                                                                                                                                                                                                                                                   *Transcription nuclei late in
                                                                                                                                                                                                                                                               nuclei late in an acute phase response elements.";
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                               MEDLINE $\,96102059; PubMed $\,8530402; Ripperger J.A., Fritz S., Richter
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID~10116;
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                                                                                                                                                                                                                                                     Biol.
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           MEMBER (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR: TRANSLOCATED INTO THE NUCLEUS IN RESPONSE TO PHOSPHORYLATION (BY SIMILARITY).

PTM: TYROSINE PHOSPHORYLATED (BY SIMILARITY).

SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYPPNPDSVLD -- TDGD ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMDLTSECA
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Pfam; PF01017; STAT; 1.
SMART; SM00252; SH2; 1.
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InterPro; IPR001217; STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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European Bioinformatics Institute.
               --TTKRGLSIEQLTTLAEKLLGPGVN----YSGCQITWAKFCKENMAGKGFSFWVWLDNI
                                              KTLSLPVVVIVHGSQDNNATATVLWDNAF-REPGRVP-FAVPDKVLWPQLCEALNMKFKA
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X91988;
X97541;
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                                                                                                              HQA-TGTLSAHFRNMSLK--RIKRSDRRGAES---VTEEKFTILFDSQFSVGGNELVFQV
                                                                                                                                                                                                                                               EHLCQQLPIPG-PVEEMLAEVNATITDIISALSTSTFIIEKQP------PQVLKTQTK
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L -> A (IN REF. 2).
S -> V (IN REF. 2).
R -> A (IN REF. 2).
R -> A (IN REF. 2).
R -> A (IN REF. 2).
T -> A (IN REF. 2).
T -> A (IN REF. 2).
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Pred. No. 8.
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                                                                                       entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhu M. H., John S., Berg M., Leonard W.J.;
"Functional association of Nmi with Stat5 a
IFNgamma-mediated signaling.";
Cell 96:121-130(1999).
-I- FUNCTION: CARRIES OUT A DUAL FUNCTION:
ACTIVATION OF TRANSCRIPTION. BINDS TO 7
ACTIVATES PRL-INDUCED TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P51692;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPT
STAT5B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96210005; PubMed-8631883;
Lin J.-X., Mietz J., Modi W.S., John S., Leonard
"Cloning of human Stat5B. Reconstitution of inter
Stat5A and Stat5B DNA binding activity in COS-7 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Buropean Bioinformatics Institute. There are no restricted to the second control of the second control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELAT MEMBER (BY SIMILARITY). INTERRCTS WITH NMI.
SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED INTO THE NUC RESPONSE TO PHOSPHORYLATION (BY SIMILARITY).
PTM: TYROSINE PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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                                                                                                                                                                              non-profit institutions as long and this statement is not removed.
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Transcription regulation; DN
Phosphorylation; SH2 domain.
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686
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InterPro; IPR001217;
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  SQERMFWNLMPFTTRDFSIRSLAD----
                                                                                           EVQSNRGLTKENLVFLAQKLFNNSSSHLEDYSGLSVSWSQFNRENLPGRNYTFWQWFDGV
                                                                                                                                           KTLSLPVVVIVHGSQDNNATATVLWDNAFA-EPGRVP-FAVPDKVLWPQLCEALNMKFKA
                                                                                                                                                                  ETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQF;S
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                                                             IDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDI
                                                                                                                      --TTKRGLSIEQLTTLAEKLLGPG---
                                                                                                                                                                                            HQA-TGTLSAHFRNMSLK--RIKRSDRRGAES---VTEEKFTILFESQFSVGGNELVFQV
                                                                                                                                                                                                                    EESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQG--LKIDL
                                                                                                                                                                                                                                               FAATVRLLVG-
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P42224;
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SIMILARITY).
REQUIRED FOR INTERACTION W
A -> P (IN REF. 2).
S -> T (IN REF. 2).
D -> DA (IN REF. 2).
R -> G (IN REF. 2).
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-> G (IN REF. 2)
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RESULT 15
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Pfam; PF01017; STAT; 1.
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EMBL; U43185;
HSSP; P42224;
MIM; 601511;
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MEDLINE-95236592; PubMed-7719937;
HOU J., Schindler U., Henzel W.J., W
"Identification and purification of response to interleukin 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin J.X., Metz J., Modi W.S., John S., Leonard W.J.;
Submitted ..BC-19°5) to the EMBL/GenBank/DBJ databases.
-i- FUNCT:-U-: CARKLES OUT A DUAL FUNCTION: SIGNAL TRANSDUCTION
ACTIVATION OF TRANSCRIPTION. BINDS TO THE GAS ELEMENT AND
                                                                                                                                                                       Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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SUBCELLULAR LOCATION: NUCLEAR; TRANSLOCATED RESPONSE TO PHOSPHORYLATION.
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PHOSPHORYLATION PHOSPHORYLATION G -> R (IN REF.
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Best Local Similarity 30.4%; Pred. No. 1.3e-4b;
Matches 248; Conservative 146; Mismatches 316; Indels 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 REANNCSSPAG----ILVDAMSQKHLQINQTFEELRLVTQDTENELKKLQQTQEYFIIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LEGLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQKTYDRCPLELVRCIRHILYNEQRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYA----ASKESHATLV 56
NPDHVLD--QDGE------FDLDETMDVA 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KTLKSQGDMQDL-----NGNNQSVTRQKMQQLEQML----TALDQMRRSIVSELAGL 224
                                                        PVLAKAVDGYVKPQIKQVVPEFVNASADAGGSSATYMDQ---APSPAVCPQA-PYNMYPQ
                                                                                                                SPERNLWNLKPFTTRDFSIRSLAD-----RLGD-----LSYLIYVFPDRPKDEVFSKYYT
                                                                                                                                    SGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCR 688
                                                                                                                                                                           MEVLKKHHKPH:/NDGAILGEVNKQQAHDLLINKEDGTFLLRESD-SEIGGIT1AW--KFD
                                                                                                                                                                                          IDLVKKYILALMNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDI 628
                                                                                                                                                                                                                                       EVQSNRGLTKENLVFLAQKLFNNSSSHLEDYSGLSVSWSQFNRENLPGWNYTFWQWFDGV
                                                                                                                                                                                                                                                                   --TTKRGLSIEQLTTLAEKLLGPG----VNYSGCQITWAKFCKENMAGKGFSFWVWLDNI 568
                                                                                                                                                                                                                                                                                               ETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSS
                                                                                                                                                                                                                                                                                                                                                         HQA-TGTLSAHFRNMSLKRIK-----RADRRGAESVTEEKFTVLFESQFSVGSNELVFQV
                                                                                                                                                                                                                                                                                                                                                                                EESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETE--VYHQGLKIDL
                                                                                                                                                                                                                                                                                                                                                                                                                    FAATVRLLVG-GKLNVHMNPPQVKATIISEQQAKSLLKNENTRNECSGEIL-NNCCVMEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTTKVRLLVKFPELNYQL---KIKVCIDKDSGDVAALRGSRKFN-----ILGTNTKVMNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EHLCQQLPIPG-PVEEMLAEVNATITDIISALVTSTFIIEKQP------PQVLKTQTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQLLRKQQTIILDDELIQWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSAMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QESTRIOAGEAGTAGESPOERTSRETALQQKQVSTEAMTQREAGTLQQYRVELAEKHQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              794 AA;
                                                                                  ----SQEHPE-----ADP-GSAAPYLKTKFICVTPTTCSNTIDLPMSPR 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90647 MW; C64237295F88CFBE CRC64;
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Search completed: March 19, 2002, 15:24:25 Job time: 287 sec